

GenCore version 5.1.7  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 17, 2006, 09:42:00 ; Search time 25.6 Seconds

(without alignments)  
96.114 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGAAAAACAGACTCATTTGGC 28

Scoring table: BLOSUM62

Xgapext 0.5  
Ygapop 10.0 ' Ygapext 0.5  
Pgapop 6.0 ' Pgapext 7.0  
Delop 6.0 ' Delext 7.0

Searched: 244313 seqs, 4393781 residues

Total number of hits satisfying chosen parameters:

4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL:frame+ n2p model -DB=abes/ABESWEB spool /runat\_16022006\_160649\_2198/app\_query.fasta \_1  
-DB=A Geneseq -QMT=Fastan -SUFIXX=ag -MINMATCH=0.1 -LOOPCII=0 -LIST=5  
-UNITS-bits -START=1 -END=1 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNS=15 -MODE=LOCAL  
-OUTFILE=pro -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=20000000000 -HOST=abes02p  
-USER=US10717243 @CGN 1-1 348 -@runat\_16022006\_160649\_2198 -NCPU=6 -ICPU=3  
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7

Database : A\_Geneseq\_21:\*

1: geneseqP1980s:\*

2: geneseqP1990s:\*

3: geneseqP2000s:\*

4: geneseqP2001s:\*

5: geneseqP2002s:\*

6: geneseqP2003s:\*

7: geneseqP2004s:\*

8: geneseqP2005s:\*

9: geneseqP2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	53	100.0	251	2	AAR63923	Arabidopsis
C 2	45	84.9	132	3	AAG59355	Arabidopsis
C 3	45	84.9	190	3	AAG59354	Arabidopsis
C 4	45	84.9	196	3	AAG60327	Arabidopsis
C 5	45	84.9	220	3	AAG59642	Arabidopsis
C 6	45	84.9	257	3	AAG60333	Arabidopsis
C 7	45	84.9	263	3	AAG60326	Arabidopsis
C 8	45	84.9	286	3	AAG64861	Arabidopsis
C 9	45	84.9	287	3	AAG59641	Arabidopsis

C 10	45	84.9	315	3	AAG60332	Arabidopsis
C 11	45	84.9	321	3	AAG60325	Arabidopsis
C 12	45	84.9	327	3	AAG60331	Arabidopsis
C 13	45	84.9	344	3	AAG60330	Arabidopsis
C 14	45	84.9	345	3	AAG59860	Arabidopsis
C 15	45	84.9	356	3	AAG59640	Arabidopsis
C 16	43	81.1	235	2	AAR63913	Type I RI
					Aar37291	plant typ
					Aar63903	Type I ri
					Aar63914	Type I RI
					Aar63922	Type I RI
					Aar63916	Type I RI
					Aar63921	Type I RI
					Aar63917	Type I RI
					Aar63918	Type I RI
					Aar63920	Type I RI
					Aar63915	Type I RI
					Aar63919	Type I RI
					Aar63924	Type I RI
					Aar63912	Type I RI
					Aar74177	Type I ri
					AdG63044	Gelonium
					Aaw29300	BPI peptide
					Aaw29303	BPI peptide
					Abg71551	G multif
					Aaw29294	BPI peptide
					Abg68722	scrV23-qe
					Abg71552	Murine sc
					Abg73777	Human col
					Abp64462	Human ORF
					Ab000814	PolyPepI
					Aar22227	Gelonin t
					Ab000515	Novel hum
					Abg71552	Murine sc
					Abg73777	Human col
					Abp64462	Human ORF
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	</					

XX PS Example 3; Page 187-188; 221pp; English.

XX AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. CC RIPS are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targeted, by the specific binding capability of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 251 AA;

Alignment Scores:	Length: 251
Pred. No.:	Matches: 9
Score: 53.00	Conservative: 0
Percent Similarity: 100.0%	Mismatches: 0
Best Local Similarity: 100.0%	Indels: 0
Query Match: 100.0%	Gaps: 0
DB: 2	

US-10-717-243-59 (1-28) x AAR63923 (1-251)

Qy 2 ACATGAAACAGAGCTTCAATTGGC 28

Db 102 ThrcyBlysThrArgLeuHisPheGly 110

RESULT 2

ID AAG5355 standard; protein; 132 AA.

XX AAG5355;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 76769.

XX KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP103405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 05-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 06-APR-1999; 99US-0125788P.

PR 08-APR-1999; 99US-0128234P.

PR 16-APR-1999; 99US-0128144P.

PR 19-APR-1999; 99US-0129845P.

PR 21-APR-1999; 99US-0130407P.

PR 25-MAR-1999; 99US-0126564P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128910P.

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Alignment Scores:  
 Pred. No.: 7.45 Length: 190  
 Score: 45.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 87.5% Mismatches: 0  
 Query Match: 84.9% Deletions: 0  
 DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x AAG59354 (1-190)

Qy 25 AAAATGAGTCCTGTTACATGT 2  
 ID AAG60327 standard; protein; 196 AA.  
 AC AAG60327;  
 XX  
 DB Arabidopsis thaliana protein fragment SEQ ID NO: 78128.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PR 25-FEB-2000; 20000EP-00301439.  
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 PR 01-APR-1999; 99US-0127442P.  
 PR 23-APR-1999; 99US-0128234P.  
 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
 PR 19-APR-1999; 99US-0130077P.  
 PR 21-APR-1999; 99US-0130449P.  
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 PR 28-APR-1999; 99US-0131449P.  
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 PR 07-MAY-1999; 99US-0132853P.  
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PR 25-OCT-1999; 99US-0161405P.  
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 06-AUG-1999; 99US-0147416P.  
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 17-AUG-1999; 99US-0149175P.  
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Alignment Scores:  
 Pred. No.: 7.46  
 Score: 45.00  
 Percent Similarity: 100.0%  
 Best Local Similarity: 87.5%  
 Query Match: 84.9%  
 DB: 3  
 XX

Length: 196  
 Matches: 7  
 Conservative: 1  
 Mismatches: 0  
 Deletions: 0  
 Gaps: 0

US-10-717-243-59 (1-28) x AAG60327 (1-196)

Qy 25 AAAATGAAAGCTCTGTTTACATGT 2  
 Db 81 LysMetLysAlaCysPheThrCys 88

RESULT 5  
 AAG59642  
 ID AAG59642 standard; protein; 220 AA.  
 XX  
 XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 77166.

KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 XX 06-SEP-2000.  
 PD 06-SEP-2000.  
 XX  
 XX 25-FEB-2000; 2000EP-00301439.  
 PF 25-FEB-1999; 99US-0121825P.  
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PR	22-JUL-1999;	99US-0144332P.	PR	21-OCT-1999;	99US-016815P.
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PR	28-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-016989P.



PR 02-AUG-1999; 99US-0146388P. PR 02-AUG-1999; 99US-0146388P. PR 02-AUG-1999; 99US-0146388P. PR 03-AUG-1999; 99US-0147038P. PR 04-AUG-1999; 99US-0147204P. PR 04-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147192P. PR 06-AUG-1999; 99US-0147303P. PR 06-AUG-1999; 99US-0147416P. PR 09-AUG-1999; 99US-0147433P. PR 10-AUG-1999; 99US-0147935P. PR 11-AUG-1999; 99US-0148319P. PR 12-AUG-1999; 99US-0148341P. PR 13-AUG-1999; 99US-0148565P. PR 13-AUG-1999; 99US-0148684P. PR 16-AUG-1999; 99US-0149368P. PR 17-AUG-1999; 99US-0149115P. PR 18-AUG-1999; 99US-0149436P. PR 20-AUG-1999; 99US-0149722P. PR 20-AUG-1999; 99US-0149723P. PR 23-AUG-1999; 99US-0149902P. PR 23-AUG-1999; 99US-0149930P. PR 25-AUG-1999; 99US-0150566P. PR 26-AUG-1999; 99US-0150884P. PR 27-AUG-1999; 99US-0151055P. PR 27-AUG-1999; 99US-0151066P. PR 27-AUG-1999; 99US-0151080P. PR 30-AUG-1999; 99US-0151303P. PR 31-AUG-1999; 99US-0151438P. PR 01-SEP-1999; 99US-0151920P. PR 07-SEP-1999; 99US-0152363P. PR 10-SEP-1999; 99US-0153070P. PR 13-SEP-1999; 99US-0153758P. PR 15-SEP-1999; 99US-0154018P. PR 16-SEP-1999; 99US-0154039P. PR 20-SEP-1999; 99US-0154779P. PR 22-SEP-1999; 99US-0155139P. PR 23-SEP-1999; 99US-0155488P. PR 24-SEP-1999; 99US-0155655P. PR 28-SEP-1999; 99US-0156458P. PR 29-SEP-1999; 99US-0156536P. PR 04-OCT-1999; 99US-0157117P. PR 05-OCT-1999; 99US-0157753P. PR 06-OCT-1999; 99US-0157855P. PR 07-OCT-1999; 99US-0158029P. PR 08-OCT-1999; 99US-0158232P. PR 12-OCT-1999; 99US-0158369P. PR 13-OCT-1999; 99US-0159233P. PR 13-OCT-1999; 99US-0159244P. PR 13-OCT-1999; 99US-0159255P. PR 14-OCT-1999; 99US-0159339P. PR 14-OCT-1999; 99US-0159310P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159637P. PR 14-OCT-1999; 99US-0159638P. PR 18-OCT-1999; 99US-0159584P. PR 21-OCT-1999; 99US-0160741P. PR 21-OCT-1999; 99US-0160747P. PR 21-OCT-1999; 99US-0160768P. PR 21-OCT-1999; 99US-0160770P. PR 21-OCT-1999; 99US-0160814P. PR 21-OCT-1999; 99US-0160815P. PR 22-OCT-1999; 99US-0160980P. PR 22-OCT-1999; 99US-0160981P. PR 22-OCT-1999; 99US-0160989P. PR 25-OCT-1999; 99US-0161405P. PR 25-OCT-1999; 99US-0161406P. PR 26-OCT-1999; 99US-0161359P. PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P. PR 28-OCT-1999; 99US-0161920P. PR 28-OCT-1999; 99US-016192P. PR 28-OCT-1999; 99US-016193P. PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:  
Pred. No.: 7.51  
Score: 45.00  
Percent Similarity: 100.0%  
Best Local Similarity: 87.5%  
Query Match: 84.9%  
DB: 3 Gaps: 0

Length: 257  
Matches: 7  
Conservative: 1  
Mismatched: 0  
Indels: 0

US-10-717-243-59 (1-28) x AAG60333 (1-257)

Qy 25 AAAATGAGTCTGGTTACATGT 2  
Db 148 LysMethylsAlaCysPheThrCys 155

RESULT 7  
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ID AAG60326 standard; protein; 263 AA.  
XX  
AC AAG60326;  
XX DT 18-OCT-2000 (first entry)  
XX DB Arabidopsis thaliana protein fragment SEQ ID NO: 78127.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.  
XX KW Arabidopsis thaliana.  
XX OS EP1033405-A2.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX XX 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
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PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
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PR 23-APR-1999; 99US-0130510P.  
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PR 14-MAY-1999; 99US-0134221P.  
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PR 18-MAY-1999; 99US-0134168P.  
PR 19-MAY-1999; 99US-0134241P.  
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PR 21-MAY-1999; 99US-0135153P.

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PR	28-MAY-1999;	99US-0136782P.	99US-0145302P.
PR	01-JUN-1999;	99US-0137222P.	99US-0145192P.
PR	03-JUN-1999;	99US-0137512P.	99US-0145260P.
PR	04-JUN-1999;	99US-0137602P.	99US-0145303P.
PR	07-JUN-1999;	99US-0137724P.	99US-014516P.
PR	08-JUN-1999;	99US-013894P.	99US-014517493P.
PR	10-JUN-1999;	99US-0138540P.	99US-01451999;
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PR	14-JUN-1999;	99US-0139119P.	PR 05-AUG-1999;
PR	16-JUN-1999;	99US-0139452P.	PR 05-AUG-1999;
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PR	18-JUN-1999;	99US-0139455P.	PR 10-AUG-1999;
PR	18-JUN-1999;	99US-0139462P.	PR 11-AUG-1999;
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PR	22-JUN-1999;	99US-0139899P.	PR 16-AUG-1999;
PR	23-JUN-1999;	99US-014015P.	PR 17-AUG-1999;
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PR	24-JUN-1999;	99US-014054P.	PR 18-AUG-1999;
PR	28-JUN-1999;	99US-014082P.	PR 20-AUG-1999;
PR	29-JUN-1999;	99US-014091P.	PR 20-AUG-1999;
PR	30-JUN-1999;	99US-0141287P.	PR 23-AUG-1999;
PR	01-JUL-1999;	99US-014184P.	PR 23-AUG-1999;
PR	01-JUL-1999;	99US-0142154P.	PR 25-AUG-1999;
PR	02-JUL-1999;	99US-0142055P.	PR 26-AUG-1999;
PR	06-JUL-1999;	99US-0142190P.	PR 27-AUG-1999;
PR	08-JUL-1999;	99US-0142803P.	PR 27-AUG-1999;
PR	12-JUL-1999;	99US-0142320P.	PR 29-AUG-1999;
PR	13-JUL-1999;	99US-0143977P.	PR 04-OCT-1999;
PR	14-JUL-1999;	99US-014354P.	PR 16-SEP-1999;
PR	15-JUL-1999;	99US-0143624P.	PR 20-SEP-1999;
PR	16-JUL-1999;	99US-0144005P.	PR 07-SEP-1999;
PR	16-JUL-1999;	99US-0144005P.	PR 24-SEP-1999;
PR	19-JUL-1999;	99US-0144086P.	PR 28-SEP-1999;
PR	19-JUL-1999;	99US-0144325P.	PR 29-SEP-1999;
PR	19-JUL-1999;	99US-0144331P.	PR 04-OCT-1999;
PR	20-JUL-1999;	99US-0144332P.	PR 13-OCT-1999;
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PR	22-JUL-1999;	99US-0144633P.	PR 14-OCT-1999;
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PR	23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;
PR	23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;
PR	26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;
PR	27-JUL-1999;	99US-014513P.	PR 25-OCT-1999;
PR	27-JUL-1999;	99US-0145192P.	PR 25-OCT-1999;
PR	27-JUL-1999;	99US-014518P.	PR 26-OCT-1999;
PR	28-JUL-1999;	99US-0145118P.	PR 26-OCT-1999;
PR	02-AUG-1999;	99US-0145386P.	PR 26-OCT-1999;
PR	02-AUG-1999;	99US-0146388P.	PR 28-OCT-1999;

PR 28-OCT-1999; 99US-0161992P.  
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 PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:  
 Pred. No.: 7.51 Length: 263  
 Score: 45.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 87.5% Mismatches: 0  
 Query Match: 84.9% Indels: 0  
 DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x AAG60326 (1-263)

Qy 25 AAAATGAACTCTGTTTACATGT 2  
 Db 148 LysMethylsAlaCysPheThrCys 155

RESULT 8  
 ID AAG04861 standard: Protein: 286 AA.  
 XX AAG04861;  
 XX DT 17-OCT-2000 (first entry)  
 XX DB Arabidopsis thaliana protein fragment SEQ ID NO: 1048.  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX OS Arabidopsis thaliana.  
 XX PN EP10334-05-A2.  
 XX PD 06-SEP-2000.  
 XX PF 25-FEB-2000; 2000EP-00301439.  
 XX 25-FEB-1999; 39US-0121845P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126244P.  
 PR 29-MAR-1999; 99US-0126755P.  
 PR 01-APR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128244P.  
 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
 PR 19-APR-1999; 99US-0130077P.  
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 PR 04-JUN-1999; 99US-0137724P.  
 PR 07-JUN-1999; 99US-0138094P.  
 PR 08-JUN-1999; 99US-0138540P.  
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 PR 01-JUL-1999; 99US-0141842P.  
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 PR 02-JUL-1999; 99US-014055P.  
 PR 06-JUL-1999; 99US-0143390P.  
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 PR 21-JUL-1999; 99US-0145218P.  
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 PR 02-AUG-1999; 99US-0145388P.  
 PR 02-AUG-1999; 99US-0145389P.  
 PR 03-AUG-1999; 99US-0147038P.

PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-014702P.	Alignment Scores:	7.53	Length: 286
PR	05-AUG-1999;	99US-0147192P.	Pred. No.:	45.00	Matches: 7
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PR	06-AUG-1999;	99US-014703P.	Percent Similarity:	87.5%	Mismatches: 0
PR	06-AUG-1999;	99US-0147161P.	Best Local Similarity:	84.9%	Indels: 0
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PR	10-AUG-1999;	99US-014817P.			
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PR	17-AUG-1999;	99US-014917P.	RESULT 9		
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PR	23-AUG-1999;	99US-0149902P.	AC		
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PR	26-AUG-1999;	99US-0150884P.	XX		
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PR	31-AUG-1999;	99US-0151438P.	XX		
PR	01-SEP-1999;	99US-0151530P.	XX		
PR	07-SEP-1999;	99US-0152263P.	XX		
PR	10-SEP-1999;	99US-0153070P.	XX		
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PR	21-OCT-1999;	99US-0160814P.	PR	07-MAY-1999;	99US-0134768P.
PR	25-OCT-1999;	99US-0161405P.	PR	18-MAY-1999;	99US-0134941P.
PR	26-OCT-1999;	99US-0161406P.	PR	19-MAY-1999;	99US-0134256P.
PR	26-OCT-1999;	99US-0160980P.	PR	20-MAY-1999;	99US-0134218P.
PR	22-OCT-1999;	99US-0160981P.	PR	21-MAY-1999;	99US-0134219P.
PR	22-OCT-1999;	99US-0160989P.	PR	14-MAY-1999;	99US-0134221P.
PR	25-OCT-1999;	99US-0161404P.	PR	14-MAY-1999;	99US-0134370P.
PR	25-OCT-1999;	99US-0161405P.	PR	18-MAY-1999;	99US-0134768P.
PR	26-OCT-1999;	99US-0161406P.	PR	19-MAY-1999;	99US-0134941P.
PR	26-OCT-1999;	99US-0161360P.	PR	20-MAY-1999;	99US-013621P.
PR	26-OCT-1999;	99US-0161361P.	PR	24-MAY-1999;	99US-013629P.
PR	28-OCT-1999;	99US-0161920P.	PR	25-MAY-1999;	99US-013621P.
PR	28-OCT-1999;	99US-0161922P.	PR	27-MAY-1999;	99US-0136392P.
PR	28-OCT-1999;	99US-016193P.	PR	28-MAY-1999;	99US-0136782P.

PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139452P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0148368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0148175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0148426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0148722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0148929P.
PR	18-JUN-1999;	99US-0139459P.	PR	23-AUG-1999;	99US-0148902P.
PR	21-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0148930P.
PR	22-JUN-1999;	99US-0139461P.	PR	25-AUG-1999;	99US-0150566P.
PR	23-JUN-1999;	99US-0139462P.	PR	26-AUG-1999;	99US-0150884P.
PR	23-JUN-1999;	99US-0139463P.	PR	27-AUG-1999;	99US-0151065P.
PR	24-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151066P.
PR	28-JUN-1999;	99US-0140833P.	PR	27-AUG-1999;	99US-0151080P.
PR	29-JUN-1999;	99US-0140991P.	PR	30-AUG-1999;	99US-0151303P.
PR	30-JUN-1999;	99US-0141287P.	PR	31-AUG-1999;	99US-0151438P.
PR	01-JUL-1999;	99US-0141844P.	PR	01-SEP-1999;	99US-0151930P.
PR	01-JUL-1999;	99US-0142054P.	PR	07-SEP-1999;	99US-0152363P.
PR	02-JUL-1999;	99US-0142055P.	PR	10-SEP-1999;	99US-0152070P.
PR	06-JUL-1999;	99US-0142330P.	PR	13-SEP-1999;	99US-0152758P.
PR	08-JUL-1999;	99US-0142803P.	PR	15-SEP-1999;	99US-0153018P.
PR	09-JUL-1999;	99US-0142920P.	PR	16-SEP-1999;	99US-0153039P.
PR	12-JUL-1999;	99US-0142977P.	PR	20-SEP-1999;	99US-0154779P.
PR	13-JUL-1999;	99US-0143542P.	PR	01-OCT-1999;	99US-0155139P.
PR	14-JUL-1999;	99US-0143624P.	PR	02-OCT-1999;	99US-0155486P.
PR	15-JUL-1999;	99US-0144005P.	PR	03-OCT-1999;	99US-0156559P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158229P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144335P.	PR	12-OCT-1999;	99US-0158330P.
PR	19-JUL-1999;	99US-0144354P.	PR	14-OCT-1999;	99US-0158469P.
PR	20-JUL-1999;	99US-0144612P.	PR	13-OCT-1999;	99US-0159393P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159338P.
PR	22-JUL-1999;	99US-0145088P.	PR	18-OCT-1999;	99US-0159545P.
PR	21-JUL-1999;	99US-0145145P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	22-OCT-1999;	99US-0160767P.
PR	23-JUL-1999;	99US-0145218P.	PR	21-OCT-1999;	99US-016089P.
PR	23-JUL-1999;	99US-0145224P.	PR	25-OCT-1999;	99US-0161404P.
PR	26-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160814P.
PR	27-JUL-1999;	99US-0145912P.	PR	25-OCT-1999;	99US-016106P.
PR	27-JUL-1999;	99US-0145913P.	PR	26-OCT-1999;	99US-016139P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-016160P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-016161P.
PR	03-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-016193P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.

Alignment Scores:  
 Pred. No. : 7.53 Length: 287  
 Score: 45.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 87.5% Mismatches: 0  
 Query Match: 84.9% Indels: 0  
 DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x AAG69641 (1-287)

Qy 25 AAAATGAACTCTGTTACATGT 2  
 XX |||||:::|||||||  
 Db 148 LysMethylAlaCysPheThrCys 155

RESULT 10

AAG69641 standard; protein; 315 AA.  
 XX  
 AC AAG69641  
 XX DT 18-OCT-2000 (first entry)

DE **Arabidopsis thaliana** protein fragment SEQ ID NO: 78135 .

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 KW XX  
 OS **Arabidopsis thaliana**.  
 PN EP10334 05-A2.  
 XX PD 06-SEP-2000.  
 XX PF 25-FEB-2000; 2000EP-00301439.  
 XX PR 25-FEB-1999; 99US-0121825P.  
 PR 09-MAR-1999; 99US-0123180P.  
 PR 23-MAR-1999; 99US-0123348P.  
 PR 25-MAR-1999; 99US-0125788P.  
 PR 29-MAR-1999; 99US-0126264P.  
 PR 01-APR-1999; 99US-0126798P.  
 PR 06-APR-1999; 99US-0128462P.  
 PR 08-APR-1999; 99US-0128334P.  
 PR 16-APR-1999; 99US-0128714P.  
 PR 19-APR-1999; 99US-0130077P.  
 PR 21-APR-1999; 99US-0130449P.  
 PR 23-APR-1999; 99US-0130510P.  
 PR 28-APR-1999; 99US-0130891P.  
 PR 30-APR-1999; 99US-0131449P.  
 PR 04-MAY-1999; 99US-0132407P.  
 PR 05-MAY-1999; 99US-0132448P.  
 PR 14-MAY-1999; 99US-0134218P.  
 PR 06-MAY-1999; 99US-0134449P.  
 PR 07-MAY-1999; 99US-0132486P.  
 PR 11-MAY-1999; 99US-0134256P.  
 PR 14-MAY-1999; 99US-0134484P.  
 PR 14-MAY-1999; 99US-0135124P.  
 PR 21-MAY-1999; 99US-013555P.  
 PR 25-MAY-1999; 99US-0135629P.  
 PR 27-MAY-1999; 99US-0136021P.  
 PR 01-JUN-1999; 99US-0136782P.  
 PR 03-JUN-1999; 99US-0137528P.

XX DE 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0138119P.  
 PR 16-JUN-1999; 99US-0138452P.  
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 PR 17-JUN-1999; 99US-0138459P.  
 PR 18-JUN-1999; 99US-0138460P.  
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 PR 18-JUN-1999; 99US-0138750P.  
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 PR 21-JUN-1999; 99US-0138817P.  
 PR 22-JUN-1999; 99US-0138899P.  
 PR 23-JUN-1999; 99US-014053P.  
 PR 23-JUN-1999; 99US-0140534P.  
 PR 24-JUN-1999; 99US-0140695P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141384P.  
 PR 01-JUL-1999; 99US-014154P.  
 PR 02-JUL-1999; 99US-014055P.  
 PR 06-JUL-1999; 99US-0141390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
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 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
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 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0144866P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0144335P.  
 PR 23-JUL-1999; 99US-0144352P.  
 PR 23-JUL-1999; 99US-0144632P.  
 PR 26-JUL-1999; 99US-0144877P.  
 PR 27-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 27-JUL-1999; 99US-0145919P.  
 PR 28-JUL-1999; 99US-0145951P.  
 PR 02-AUG-1999; 99US-0145386P.  
 PR 02-AUG-1999; 99US-0145388P.  
 PR 02-AUG-1999; 99US-0145389P.  
 PR 03-AUG-1999; 99US-0145388P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 04-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147260P.

PR 06-AUG-1999; 99US-0147303P. Score: 45.00  
 PR 06-AUG-1999; 99US-0147416P. Percent: Similarity: 100.0%  
 PR 09-AUG-1999; 99US-0147493P. Best Local Similarity: 97.5%  
 PR 09-AUG-1999; 99US-0147935P. Mismatches: 1  
 PR 10-AUG-1999; 99US-0148177P. Query Match: 84.9%  
 PR 11-AUG-1999; 99US-0148319P. DB: 3  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148568P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149366P.  
 PR 17-AUG-1999; 99US-0149174P.  
 PR 18-AUG-1999; 99US-0149436P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149928P.  
 PR 23-AUG-1999; 99US-0149904P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151063P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151084P.  
 PR 30-AUG-1999; 99US-0154018P.  
 PR 31-AUG-1999; 99US-0151430P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153756P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154038P.  
 PR 20-SEP-1999; 99US-0154775P.  
 PR 22-SEP-1999; 99US-0155133P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0155655P.  
 PR 28-SEP-1999; 99US-0156455P.  
 PR 29-SEP-1999; 99US-0156598P.  
 PR 04-OCT-1999; 99US-0157110P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158020P.  
 PR 08-OCT-1999; 99US-0158233P.  
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 PR 21-OCT-1999; 99US-0159741P.  
 PR 22-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
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 PR 25-OCT-1999; 99US-0161400P.  
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 PR 26-OCT-1999; 99US-0161355P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161367P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161990P.  
 PR 29-OCT-1999; 99US-0162144P.  
 PR 29-OCT-1999; 99US-0162144P.

Matches: 7  
 Conservative: 1  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-10-717-243-59 (1-28) x AAG60332 (1-315)

Qy 25 AAAATGAGTCTTACATGT 2  
 Db 206 LysMethylsAlaCysPheThrCys 213

RESULT 11  
 AAG60325  
 ID AAG60325 standard; protein; 321 AA.  
 XX  
 AC AAG60325;  
 XX  
 DT 18-OCT-2000 (first entry)  
 XX  
 Arabidopsis thaliana protein fragment SEQ ID NO: 78126.  
 DE XX  
 KW XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS XX  
 XX  
 PR 01-SEP-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 09-MAR-1999; 99US-0125788P.  
 PR 23-MAR-1999; 99US-0126264P.  
 PR 25-MAR-1999; 99US-0126785P.  
 PR 29-MAR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128234P.  
 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
 PR 19-APR-1999; 99US-0130077P.  
 PR 21-APR-1999; 99US-013049P.  
 PR 23-APR-1999; 99US-0130510P.  
 PR 01-APR-1999; 99US-0130891P.  
 PR 06-MAY-1999; 99US-0131449P.  
 PR 28-APR-1999; 99US-0132487P.  
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 PR 30-APR-1999; 99US-0132407P.  
 PR 11-MAY-1999; 99US-0132456P.  
 PR 14-MAY-1999; 99US-0132484P.  
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 PR 14-MAY-1999; 99US-0132487P.  
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 PR 01-JUN-1999; 99US-0132487P.  
 PR 03-JUN-1999; 99US-0132487P.  
 PR 04-JUN-1999; 99US-0132487P.  
 PR 07-JUN-1999; 99US-0132487P.

Length: 315

Alignment Scores:  
 Pred. No.: 7.55

PR	08-JUN-1999;	99US-0138094P.	99US-0147493P.
PR	10-JUN-1999;	99US-0138854P.	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	99US-0147939P.
PR	14-JUN-1999;	99US-0139119P.	99US-0147171P.
PR	16-JUN-1999;	99US-0139452P.	99US-0148319P.
PR	16-JUN-1999;	99US-0139453P.	99US-0148341P.
PR	17-JUN-1999;	99US-0139492P.	99US-0148565P.
PR	18-JUN-1999;	99US-013954P.	99US-0148684P.
PR	18-JUN-1999;	99US-013955P.	99US-0148688P.
PR	18-JUN-1999;	99US-0139456P.	99US-0148426P.
PR	18-JUN-1999;	99US-0139457P.	99US-0148722P.
PR	18-JUN-1999;	99US-0139458P.	99US-0148723P.
PR	18-JUN-1999;	99US-0139459P.	99US-0148929P.
PR	18-JUN-1999;	99US-0139460P.	99US-0148902P.
PR	18-JUN-1999;	99US-0139461P.	99US-0148930P.
PR	18-JUN-1999;	99US-0139462P.	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	99US-0150884P.
PR	18-JUN-1999;	99US-0139475P.	99US-0151065P.
PR	18-JUN-1999;	99US-0139499P.	99US-0148929P.
PR	21-JUN-1999;	99US-0139817P.	99US-014899P.
PR	22-JUN-1999;	99US-0139899P.	99US-0151303P.
PR	23-JUN-1999;	99US-0139899P.	99US-0151438P.
PR	23-JUN-1999;	99US-014053P.	99US-0151930P.
PR	24-JUN-1999;	99US-014054P.	99US-0151936P.
PR	28-JUN-1999;	99US-0140615P.	99US-0152070P.
PR	28-JUN-1999;	99US-0139763P.	99US-0152070P.
PR	29-JUN-1999;	99US-0140823P.	99US-0152758P.
PR	30-JUN-1999;	99US-014091P.	99US-0153080P.
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PR	01-JUL-1999;	99US-0141642P.	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	99US-0154139P.
PR	02-JUL-1999;	99US-0142055P.	99US-0154266P.
PR	06-JUL-1999;	99US-014239P.	99US-0154659P.
PR	08-JUL-1999;	99US-0142803P.	99US-0154758P.
PR	09-JUL-1999;	99US-014299P.	99US-015496P.
PR	12-JUL-1999;	99US-0143142P.	99US-0157117P.
PR	13-JUL-1999;	99US-014331P.	99US-0157753P.
PR	14-JUL-1999;	99US-014342P.	99US-0157865P.
PR	15-JUL-1999;	99US-0144005P.	99US-0158029P.
PR	16-JUL-1999;	99US-0144085P.	99US-0158239P.
PR	16-JUL-1999;	99US-0144098P.	99US-0158330P.
PR	19-JUL-1999;	99US-014425P.	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	99US-0159295P.
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Alignment Scores:

Pred. No. :

Score:

Percent Similarity:

Length:

Matches:

Conservative:

7.55

45.00

100.0%

Best Local Similarity: 87.5% Mismatches: 0  
 Query Match: 84.9% Indels: 0  
 DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x AAG60325 (1-321)

Qy 25 AAAATGAGTCCTGTTACATGT 2  
 Db 206 LysMetLeuAlaCysPheThrCys 213

RESULT 12

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 AC AAG60325;  
 XX DT 18-OCT-2000 (first entry)  
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 78134.  
 XX DE Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX OS Arabidopsis thaliana.  
 XX PN EP1033405-A2.  
 XX PD 06-SEP-2000.  
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Alignment Scores:  
Pred. No.: 7.56  
Score: 45.00  
Percent Similarity: 100.0%  
Best Local Similarity: 87.5%  
Query Match: 84.9%  
DB: 3

Length: 344  
Matches: 7  
Conservative: 1  
Mismatched: 0  
Indels: 0  
Gaps: 0

US-10-717-243-59 (1-28) x AAG04860 (1-344)

Qy 25 AAATGAGCTCTGTTACATGT 2  
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RESULT 14

AAG59640

ID AAG59640 standard; protein; 345 AA.

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AC AAG59640;

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DT 18-OCT-2000 (first entry)

DB Arabidopsis thaliana protein Fragment SEQ ID NO: 77164.

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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

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OS Arabidopsis thaliana .

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PR 01-JUL-1999; 99US-0142154P.

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PR 13-AUG-1999; 99US-0148656P.

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PR	07-SEP-1999;	99US-0152363P.	XX		
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PR	22-OCT-1999;	99US-0160768P.	PR	06-MAY-1999;	99US-0132486P.
PR	23-OCT-1999;	99US-0160770P.	PR	06-MAY-1999;	99US-0132487P.
PR	25-OCT-1999;	99US-0160814P.	PR	07-MAY-1999;	99US-0132463P.
PR	25-OCT-1999;	99US-0160815P.	PR	11-MAY-1999;	99US-0134456P.
PR	26-OCT-1999;	99US-0160988P.	PR	14-MAY-1999;	99US-0134218P.
PR	26-OCT-1999;	99US-0161365P.	PR	14-MAY-1999;	99US-0134219P.
PR	28-OCT-1999;	99US-0161404P.	PR	24-MAY-1999;	99US-0135629P.
PR	28-OCT-1999;	99US-0161405P.	PR	25-MAY-1999;	99US-0136021P.
PR	28-OCT-1999;	99US-0161920P.	PR	27-MAY-1999;	99US-0136312P.
PR	28-OCT-1999;	99US-0161999P.	PR	28-MAY-1999;	99US-0136782P.
PR	29-OCT-1999;	99US-0162142P.	PR	01-JUN-1999;	99US-013722P.
PR			PR	03-JUN-1999;	99US-013753P.
PR			PR	04-JUN-1999;	99US-0137502P.
PR			PR	07-JUN-1999;	99US-0137724P.
PR			PR	08-JUN-1999;	99US-013804P.
PR			PR	10-JUN-1999;	99US-0138340P.
PR			PR	10-JUN-1999;	99US-0138847P.
PR			PR	14-JUN-1999;	99US-0139119P.
PR			PR	16-JUN-1999;	99US-0139452P.
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PR			PR	17-JUN-1999;	99US-0139452P.
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 Percent Similarity: 100.0%  
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 US-10-717-243-59 (1-28) x AAG59640 (1-345)



Db 21.8 LysMetLysAlaCysPheThrCys 225

Search completed: February 17, 2006, 09:46:27  
Job time : 130 secs

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NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
SEQUENCE FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-108

Alignment Scores:
Pred. No.: 0.0135 Length: 251
Score: 53.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Inels: 0
DB: 1 Gaps: 0

US-10-717-243-59 (1-28) * US-08-425-336-108 (1-251)
Qy 2 ACATGTAAACAAAGACTTCATTGGGC 28
Db 102 ThrcyslysthrArgLeuHispheGly 110

RESULT 2
US-08-488-113B-108
Sequence 108, Application US/08488113B
Patient No. 574580

GENERAL INFORMATION:
APPLICANT: Better, Marc D. F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

```

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-477-484B-108

Alignment Scores:  
 Pred. No.: 0.0135 Length: 251  
 Score: 53.00 Matches: 9  
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 DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-646-360-108 (1-251)

Qy 2 ACATGTAACACAAGACTTCATTGGC 28  
 Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 4  
 US-08-446-360-108  
 Sequence 108 Application 'US/08646360  
 Patent No. 5837491  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnicka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-360-108

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 Pred. No.: 0.0135 Length: 251  
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US-10-717-243-59 (1-28) x US-08-646-360-108 (1-251)

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 Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 5  
 US-08-839-765-108  
 Sequence 108, Application US/08839765  
 Patent No. 6146631  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnicka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
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 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
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 FILING DATE: 15-APR-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/425,336  
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 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE DOCKET NUMBER: 11022US09/200-70.P3.C3  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-839-765-108

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 Score: 53.00 Matches: 9  
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US-10-717-243-59 (1-28) x US-08-839-765-108 (1-251)

Qy 2 ACATGTAACACAGACTCATTTGGC 28  
 Db 102 ThrCysLysThrArgLeuHisPheGly 110

US-09-136-389-108

Sequence 108, Application US/09136389  
 Parent No. 6146850

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnicka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

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 OPERATING SYSTEM: PC-DOS/MS-DOS  
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 APPLICATION NUMBER: US/09/136,389  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 PRIOR APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCNICHOLAS, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70..P4

TELECOMMUNICATION INFORMATION:  
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 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-839-765-108

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 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
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US-10-717-243-59 (1-28) x US-09-136-389-108 (1-251)

Qy 2 ACATGTAACACAGACTCATTTGGC 28  
 Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 7  
 US-09-610-838-108

Sequence 108, Application US/09610838  
 Patent No. 6376217

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnicka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

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 OPERATING SYSTEM: PC-DOS/MS-DOS  
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 APPLICATION NUMBER: US/09/610,838  
 FILING DATE: 06-JUL-2000  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/136,389  
 FILING DATE: 18-AUG-1998  
 APPLICATION NUMBER: 08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: FCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCNICHOLAS, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70..P4

NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-610-838-108

Alignment Scores:  
 Pred. No.: 0.0135 Length: 251  
 Score: 53.00 Matches: 9  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x US-09-711-838-108 (1-251)

Qy 2 ACATGTAACAGACTCATTTGGC 28  
 Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 9  
 US-07-901-707-2  
 Sequence 2, Application US/07901707  
 ; Patent No. 5376546  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bernhard, Susan L.  
 ; BETTER, Marc D.  
 ; APPLICANT: Carroll, Steve F.  
 ; APPLICANT: Lane, Julie A.  
 ; TITLE OF INVENTION: Materials Comprising and Methods of  
 ; Composition and Use for Ribosome-Inactivating Proteins  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ; ADDRESSEE: Bicknell  
 ; STREET: Two First National Plaza, 20 South Clark  
 ; STREET: Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; ZIP: 60661  
 ; COUNTRY: USA  
 ; STATE: USA  
 ; ZIP: 60603  
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 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/711,485  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/639,765  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 531654 and, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27129/30910  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 346-5750  
 TELEX: (312) 984-5750  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: AMINO ACID

TOPOLGY: linear  
 MOLECULE TYPE: protein  
 US-07-901-707-2

Alignment Scores:  
 Pred. No.: 1.54 Length: 251  
 Score: 43.00 Matches: 8  
 Percent Similarity: 88.9% Conservative: 88.9%  
 Best Local Similarity: 88.9% Query Match: 81.1%  
 Query Match: 81.1% Indels: 0  
 DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-07-901-707-2 (1-251)

Qy 2 ACATGAAACAGACTCTTGC 28  
 Db 102 ThrIleLysThrArgLeuHisPheGly 110

RESULT 11  
 US-08-425-336-2

Sequence 2, Application US/08425336  
 Patent No. 5621033

GENERAL INFORMATION:  
 APPLICANT: Bernhard, Susan L.  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Lane, Julie A.  
 APPLICANT: Lei, Shau-Ping  
 TITLE OF INVENTION: Materials Comprising and Methods of  
 TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
 NUMBER OF SEQUENCES: 101  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESSEES: Bicknell  
 STREET: Two First National Plaza, 20 South Clark  
 STREET: Street:  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60603

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US/07/988,430  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US/07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 5416202 and Greta E.  
 REGISTRATION NUMBER: 35302  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 346-5750  
 TELEFAX: (312) 984-9740  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: AMINO ACID  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 US-07-901-707-2

Alignment Scores:  
 Pred. No.: 1.54 Length: 251  
 Score: 43.00 Matches: 8  
 Percent Similarity: 88.9% Conservative: 88.9%  
 Best Local Similarity: 88.9% Query Match: 81.1%  
 Indels: 0 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-2 (1-251)

Qy 2 ACATGAAACAGACTCATTTGGC 28  
 Db 102 ThrIleYsThrArgLeuHisPheGly 110

RESULT 12  
 US-08-425-336-99  
 ; Sequence 99, Application US/08425336

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 140  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/425,336  
 FILING DATE: 18-APR-1995  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/425,336  
 FILING DATE: 18-APR-1995  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 19-JUN-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Thomas C.  
 REGISTRATION NUMBER: P-36,989  
 REFERENCE/DOCKET NUMBER: 31394  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Thomas C.  
 REGISTRATION NUMBER: P-16,989  
 REFERENCE/DOCKET NUMBER: 31394  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 99:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-08-425-336-99

Alignment Scores:  
 Pred. No.: 1.54 Length: 251  
 Score: 43.00 Matches: 8  
 Percent Similarity: 88.9% Conservative: 0  
 Best Local Similarity: 88.9% Mismatches: 1  
 Query Match: 81.1% Indels: 0  
 DB: 1 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-100 (1-251)

Qy 2 ACATGAAACAGACTCATTTGGC 28  
 Db 102 ThrIleYsThrArgLeuHisPheGly 110

RESULT 13  
 US-08-425-336-100  
 ; Sequence 100, Application US/08425336  
 ; Patent No. 5621083

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 140  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois

COUNTRY: USA  
 ZIP: 60606-6402

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995  
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/064,691

FILING DATE: 11-MAY-1993  
 APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Thomas C.

REGISTRATION NUMBER: P-3-6,989  
 REFERENCE/DOCKET NUMBER: 31394

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448  
 TELEX: 25-3856

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids

TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-425-336-101

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/425,336  
 FILING DATE: 18-APR-1995  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/064,691  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Thomas C.  
 REGISTRATION NUMBER: P-3-6,989  
 REFERENCE/DOCKET NUMBER: 31394  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-10-717-243-59 (1-28) x US-08-425-336-102 (1-251)  
 Search completed: February 17, 2006, 09:53:33  
 Job time : 34 secs

Alignment Scores:  
 Pred. No.: 1.54 Length: 251  
 Score: 251 Matches: 8  
 Percent Similarity: 88.9% Conservative: 0  
 Best Local Similarity: 88.9% Mismatches: 0  
 Query Match: 81.1% Indels: 0  
 DB: 0 Gaps: 0

US-10-717-243-59 (1-28) x US-08-425-336-102 (1-251)

Qy 2 ACATGTAAGAACAGACTCATTTGGC 28  
 Db 102 ThrIleYsThrArgLeuHsPheGly 110

RESULT 15  
 US-08-425-336-102  
 Sequence 102, Application US/08425336  
 Patent No. 5621083  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 APPLICANT: Carroll, Stephen F.  
 APPLICANT: Studnicka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 TITLE OF INVENTION: Proteins  
 NUMBER OF SEQUENCES: 140  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

DM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 17, 2006, 10:07:00 ; Search time 21.7 Seconds  
(without alignments)  
107.827 Million cell updates/sec

Title: US-10-17-243-59

Perfect score: 53

Sequence: 1 CACATGTAACAAAGACTTCATTTGGC 28

Scoring table: BIOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Dgapop	6.0	Dext	7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 Summaries

Command line parameters: `WONDER-frame.n2p model.n2p -DEV-YIN`

FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32, 918  
 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
 US-10-127-89-108

Alignment Scores:  
 Pred. No.: 0.22 Length: 251  
 Score: 53.00 Matches: 9  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 4 Gaps: 0

US-10-717-243-59 (1-28) x US-10-717-243-108 (1-251)

Qy 2 ACATGTTAAACAAAGCTTCAATTGTC 28  
 Db 102 ThrCysLysThrArgLeuHisPheGly 110

RESULT 3  
 US-09-765-527-247  
 Sequence 247, Application US/09765527  
 Patent No. US2002006638A1  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
 NUMBER OF SEQUENCES: 265  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60605-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: acetylIn Release #1.0, Version #1.2.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/765,527  
 FILING DATE: 18-Jan-2001  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/621,803  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25, 447  
 REFERENCE/DOCKET NUMBER: 27129/33199  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEX: 312/474-0448  
 INFORMATION FOR SEQ ID NO: 247:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid

RESULT 2  
 US-10-717-243-108  
 Sequence 108, Application US/10717243  
 Publication No. US200501054835A1  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 Carroll, Stephen F.  
 Etudnaka, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 Proteins  
 NUMBER OF SEQUENCES: 169  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.2.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/717,243  
 FILING DATE: 18-Nov-2003  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/839,765  
 FILING DATE: 15-APR-1997  
 APPLICATION NUMBER: US 08/425,336  
 FILING DATE: 18-APR-1995  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US 07/901,707

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-127-890-2

Alignment Scores:  
 Pred. No.: 18.5 Length: 251  
 Score: 43.00 Matches: 8  
 Percent Similarity: 88.9% Conservative: 0  
 Best Local Similarity: 88.9% Mismatches: 1  
 Query Match: 81.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-2 (1-251)

Qy 2 ACATGTAACAGACTCATTTGGC 28  
 Db 102 ThrIleLysThrArgLeuHisPheGly 110

RESULT 5  
 US-10-127-890-99  
 Sequence 99, Application US/10127890  
 Publication No. US20030166196A1

GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 Carroll, Stephen F.

STUDNIKA, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 99:  
 US-10-127-890-39

Alignment Scores:

Pred. No. :	18.5	Length:	251
Score:	43.00	Matches:	8
Percent Similarity:	88.9%	Percent Similarity:	88.9%
Best Local Similarity:	88.9%	Best Local Similarity:	88.9%
Query Match:	81.1%	Query Match:	81.1%
DBs:	4	DBs:	4

US-10-717-243-59 (1-28) x US-10-127-890-99 (1-251)

Qy 2 ACATGAAACAGACTTCAATTGGC 28

Db 102 ThrIleLysThrArgLeuIlePheGly 110

RESULT 6

US-10-127-890-100

Sequence 100, Application US/10127890

Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

CARROLL, Stephen F.

STUDNIKA, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-APR-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US/08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US/07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US/07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US/07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70-P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-10-127-890-100

Alignment Scores:

Pred. No. :	18.5	Length:	251
Score:	43.00	Matches:	8

Percent Similarity: 88.9%      Conservative: 0      Indels: 0  
 Best Local Similarity: 88.9%      Mismatches: 1      Gaps: 0  
 Query Match: 81.1%      DB: 0  
 DB: 4      Insertions: 0

US-10-717-243-59 (1-28) x US-10-127-890-101 (1-251)

Qy 2 ACATGTAACAGACTCATTTGGC 28  
 Db 102 ThrIleLysThrArgLeuHisPheGly 110

RESULT 9  
 US-10-127-890-103  
 ; Sequence 103, Application US/10127890  
 ; Publication No. US2003016616A1  
 ; GENERAL INFORMATION:  
 ;      APPLICANT: Better, Marc D.  
 ;      CARROLL, Stephen F.  
 ;      STUDNIKA, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US 08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US 07/988,430  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US 07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US 07/787,567  
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70.P4

TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 102:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 102:  
 US-10-127-890-102

Alignment Scores:  
 Pred. No.: 18.5      Length: 251  
 Score: 43.00      Matches: 8  
 Percent Similarity: 88.9%      Conservative: 0  
 Best Local Similarity: 88.9%      Mismatches: 1  
 Query Match: 81.1%      Indels: 0  
 DB: 4      Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-103 (1-251)

QY 2 ACATGTAACAGACTTCATTGGC 28  
Db 102 ThrIleYstArgLeuH1sPheGly 110

RESULT 10  
US-10-127-890-104  
; Sequence 104, Application US/10127890  
; Publication No. US20030166196A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; Carroll, Stephen F.  
; STUDNIKA, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising  
; Proteins  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESS/EE: McAndrews, Held & Malloy,  
; STREET: 500 West Madison Street, 34th  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Vers  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/127, 890  
; FILING DATE: 23-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646, 360  
; FILING DATE: 13-MAY-1996  
; APPLICATION NUMBER: PCT/US94/05348  
; FILING DATE: 12-MAY-1994  
; APPLICATION NUMBER: US/08/064, 691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US/07/988, 430  
; FILING DATE: 09-DEC-1992  
; APPLICATION NUMBER: US/07/901, 707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US/07/787, 567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32, 918  
; REFERENCE/DOCKET NUMBER: 200-70-PA4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
; US-10-127-890-104  
; Alignment Scores:  
; Aligned No.: 18.5  
; Score: 43.00  
; Percent Similarity: 88.9%  
; Best Local Similarity: 88.9%  
; Query Match: 81.1%  
; DB: 4  
; Length:  
; Matches:  
; Conservative:  
; Mismatches:  
; Indels:  
; Gaps:

Qy 2 ACATGTAACAGACTTCATTGGCC 28  
 Publication No. US20030166196A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Better, Marc D.  
 / CARROLL, Stephen F.  
 / STUDNIKA, Gary M.  
 / TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
 / NUMBER OF SEQUENCES: 173  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 / STREET: 500 West Madison Street, 34th floor  
 / CITY: Chicago  
 / STATE: Illinois  
 / COUNTRY: USA  
 / ZIP: 60661  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/10/127,890  
 / FILING DATE: 23-APR-2002  
 / CLASSIFICATION: <Unknown>  
 / PRIORITY APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/646,360  
 / FILING DATE: 13-MAY-1996  
 / APPLICATION NUMBER: PCT/US94/05348  
 / FILING DATE: 12-MAY-1994  
 / APPLICATION NUMBER: US 08/064,691  
 / FILING DATE: 12-MAY-1993  
 / APPLICATION NUMBER: US 07/988,430  
 / FILING DATE: 09-DEC-1992  
 / APPLICATION NUMBER: US 07/901,707  
 / FILING DATE: 19-JUN-1992  
 / APPLICATION NUMBER: US 07/787,567  
 / FILING DATE: 04-NOV-1991  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: McNicholas, Janet M.  
 / REGISTRATION NUMBER: 32,918  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 312/707-8889  
 / TELEFAX: 312/707-9155  
 / TELEX: 650 388-1248  
 / INFORMATION FOR SEQ ID NO: 105:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 251 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
 / US-10-127-890-105  
 / Alignment Scores:  
 / Pred. No.: 18.5 Length: 251  
 / Score: 43.00 Matches: 8  
 / Percent Similarity: 88.9% Conservative: 0  
 / Best Local Similarity: 88.9% Mismatches: 1  
 / Query Match: 81.1% Index: 0  
 / DB: 4 Gaps: 0  
 / US-10-717-243-59 (1-28) x US-10-127-890-105 (1-251)  
 / 2 ACATGTAACAGACTTCATTGGCC 28

Db 102 ThrIleysThrArgLeuHisPheGly 110  
 RESULT 12 US-10-127-890-106  
 ; Sequence 106, Application US/10127890  
 ; Publication No. US20030166196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; Carroll, Stephen F.  
 ; Studnka, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 Proteins

NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60661

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US/08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US/07/988,430  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US/07/787,567  
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 REFERENCE/DOCKET NUMBER: 200-70-P4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/707-8889  
 TELEFAX: 312/707-9155  
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 106:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
 US-10-127-890-106

Alignment Scores:  
 Pred. No.: 18.5 Length: 251  
 Score: 43.00 Matches:  
 Percent Similarity: 88.9% Best Local Similarity: 88.9%  
 Best Local Similarity: 88.9% Mismatches: 1  
 Query Match: 81.1% DB: 4  
 DB: 4 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-107 (1-251)

Qy 2 ACATGAAACAGACTCATTTGGC 28  
 Db 102 ThrIleysThrArgLeuHisPheGly 110

US-10-127-890-109  
 Sequence 109, Application US/10127890  
 Publication No. US/030166136A1  
 GENERAL INFORMATION:  
 APPLICANT: Better, Marc D.  
 Carroll, Stephen F.  
 Studnika, Gary M.  
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 STREET: 500 West Madison Street, 34th floor  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60661  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/127,890  
 FILING DATE: 23-Apr-2002  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,360  
 FILING DATE: 13-MAY-1996  
 APPLICATION NUMBER: PCT/US94/05348  
 FILING DATE: 12-MAY-1994  
 APPLICATION NUMBER: US/08/064,691  
 FILING DATE: 12-MAY-1993  
 APPLICATION NUMBER: US/07/988,430  
 FILING DATE: 09-DEC-1992  
 APPLICATION NUMBER: US/07/901,707  
 FILING DATE: 19-JUN-1992  
 APPLICATION NUMBER: US/07/787,567  
 FILING DATE: 04-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McNicholas, Janet M.  
 REGISTRATION NUMBER: 32,918  
 INFORMATION FOR SEQ ID NO: 109:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 251 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
 US-10-127-890-109

Alignment Scores:  
 Pred. No.: 18.5  
 Score: 43.00  
 Percent Similarity: 88.9%  
 Best Local Similarity: 88.9%  
 Mismatches: 1  
 Query Match: 81.1%  
 DB: 4  
 Gaps: 0

US-10-717-243-59 (1-28) x US-10-127-890-110 (1-251)

Qy 2 ACATGAAACAGAGATTCAATTGGC 28  
 Db 102 ThrIleSthArgLeuHsPheGly 110

RESULTS 15  
 US-10-127-890-110, Application US/10127890

Search completed: February 17, 2006, 10:11:14  
 Job time : 108.5 secs

GenCore version 5.1.7  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 17, 2006, 10:07:45 ; Search time 2.2 Seconds  
(without alignments)

36.183 Million cell updates/sec

Title: US-10-717-243-59

Perfect score: 53

Sequence: 1 CACATGTTAAACAAAGACTTCATTGGC 28

Scoring table: BLOSUM62

Xgapext 10.0 ; Xgapext 0.5

Ygapext 10.0 ; Ygapext 0.5

Fgapext 6.0 ; Fgapext 7.0

Delop 6.0 ; Delext 7.0

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 215638

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+np2.model -DEV=xlp

-Q=/abs/ABSWEB\_spool/us10717243/runat\_16022006\_160704\_2530/app\_query.fasta\_1

-DB=Published Applications AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1

-LOPCL=-LOPEXT=0 UNITS=bites -START=1 -END=-1 -MATRIX=diamond2

-TRANS=human40.cgi -LIST=45 -DOALIGN=1 -XGAPPOP=10 -XGAPEXT=0.5

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFORMAT=txt -NORMEXT -HEARST=500 -MINLEN=0

-MAXLEN=200000000 -HOST=abs02p

-Q=/abs/ABSWEB\_spool/us10717243 @CGN 1..1..7 @runat\_16022006\_160704\_2530/app\_query.fasta\_1

-NO MMAP -NEG SCORES=0 -WAIT=0 -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published\_Applications\_AA\_New:\*

1: /cgn2\_6/ptodata/1/pubcaa/US08\_NEW\_PUB..pep:\*

2: /cgn2\_6/ptodata/1/pubcaa/US06\_NEW\_PUB..pep:\*

3: /cgn2\_6/ptodata/1/pubcaa/US07\_NEW\_PUB..pep:\*

4: /cgn2\_6/ptodata/1/pubcaa/US05\_NEW\_PUB..pep:\*

5: /cgn2\_6/ptodata/1/pubcaa/US03\_NEW\_PUB..pep:\*

6: /cgn2\_6/ptodata/1/pubcaa/US10\_NEW\_PUB..pep:\*

7: /cgn2\_6/ptodata/1/pubcaa/US11\_NEW\_PUB..pep:\*

8: /cgn2\_6/ptodata/1/pubcaa/US60\_NEW\_PUB..pep:\*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	36	67.9	13	7	US-11-116-144-68	Sequence 68, App1
c 2	36	67.9	445	7	US-11-098-686-11367	Sequence 11367, A
c 3	35	66.0	472	6	US-10-689-742-68	Sequence 68, App1
c 4	34	64.2	326	7	US-11-000-463-854	Sequence 382, App
c 5	34	64.2	326	7	US-11-000-463-854	Sequence 854, App
c 6	34	64.2	608	7	US-11-024-959-315	Sequence 315, App
c 7	33	62.3	187	6	US-10-988-388-65	Sequence 65, App1
c 8	33	62.3	522	6	US-10-519-390-21	Sequence 21, App1
c 9	33	62.3	636	7	US-11-072-512-2449	Sequence 2449, Ap

Sequence 10347, A	868	7	US-11-098-686-10347	Sequence 10347, A
Sequence 76, App1	36	7	US-11-120-308-76	Sequence 76, App1
Sequence 605, App	127	6	US-10-995-561-605	Sequence 605, App
Sequence 1372, App	211	6	US-10-821-334-1372	Sequence 1372, App
Sequence 61, App1	321	7	US-11-132-285-61	Sequence 61, App1
Sequence 3294, App	238	7	US-11-072-512-3294	Sequence 3294, App
Sequence 6782, App	273	6	US-10-467-557-6782	Sequence 6782, App
Sequence 80, App1	319	7	US-11-120-308-80	Sequence 80, App1
Sequence 82, App1	361	7	US-11-120-308-82	Sequence 82, App1
Sequence 442, App	374	6	US-10-193-676-442	Sequence 442, App
Sequence 193, App1	379	6	US-11-052-554-193	Sequence 193, App1
Sequence 22, App1	631	7	US-10-813-646-22	Sequence 22, App1
Sequence 34, App1	756	6	US-10-055-877-34	Sequence 34, App1
Sequence 187, App	756	6	US-10-055-877-187	Sequence 187, App
Sequence 188, App	756	6	US-10-055-877-189	Sequence 188, App
Sequence 32, App1	830	6	US-10-055-877-32	Sequence 32, App1
Sequence 20, App1	78	7	US-11-031-206-20	Sequence 20, App1
Sequence 11394, A	93	7	US-11-098-686-1394	Sequence 11394, A
Sequence 22, App1	132	7	US-11-031-206-198	Sequence 22, App1
Sequence 198, App	132	7	US-11-031-206-198	Sequence 198, App
Sequence 576, App	192	5	US-09-978-360-576	Sequence 576, App
Sequence 35, App1	210	7	US-11-177-509-35	Sequence 35, App1
Sequence 36, App1	210	7	US-11-177-509-36	Sequence 36, App1
Sequence 37, App1	210	7	US-11-177-509-37	Sequence 37, App1
Sequence 38, App1	210	7	US-11-177-509-38	Sequence 38, App1
Sequence 39, App1	210	7	US-11-177-509-39	Sequence 39, App1
Sequence 40, App1	210	7	US-11-177-509-40	Sequence 40, App1
Sequence 41, App1	210	7	US-11-177-509-41	Sequence 41, App1
Sequence 42, App1	210	7	US-11-177-509-42	Sequence 42, App1
Sequence 43, App1	210	7	US-11-177-509-43	Sequence 43, App1
Sequence 44, App1	210	7	US-11-177-509-44	Sequence 44, App1
Sequence 45, App1	210	7	US-11-177-509-45	Sequence 45, App1
Sequence 46, App1	210	7	US-11-177-509-46	Sequence 46, App1
Sequence 47, App1	210	7	US-11-177-509-47	Sequence 47, App1
Sequence 48, App1	210	7	US-11-177-509-48	Sequence 48, App1

#### ALIGNMENTS

RESULT 1  
US-11-116-144-68  
US-11-116-144-68  
; Sequence 68, Application US/111-16144  
; Publication US/111-16144  
; General Information:

; Applicant: BERTHET, FRANCOIS XAVIER  
; Applicant: CASABDVALI, FRANCESC VAYREDA  
; Applicant: SANCZ MARIA, MARIA CRUZ  
; Applicant: GARCIA, TERESA LLOP  
; Applicant: OLLIE, ANGELIS MOR  
; Title of Invention: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN

; Title of Invention: INFECTION  
; File Reference: INL-084  
; Current Application Number: US/11/116,144  
; Current Filing Date: 2005-04-27  
; Prior Application Number: PCT/ES04/000581  
; Prior Filing Date: 2004-12-23  
; Prior Application Number: EP 03380307.3  
; Number of SEQ ID NOS: 301  
; Software: PatentIn Ver. 3.3  
; SEQ ID NO: 68  
; Length: 13  
; Type: PRT  
; Organism: Homo sapiens  
US-11-116-144-68

Alignment Scores:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	36	67.9	13	7	US-11-116-144-68	Sequence 68, App1
c 2	36	67.9	445	7	US-11-098-686-11367	Sequence 11367, A
c 3	35	66.0	472	6	US-10-689-742-68	Sequence 68, App1
c 4	34	64.2	326	7	US-11-000-463-854	Sequence 382, App
c 5	34	64.2	326	7	US-11-000-463-854	Sequence 854, App
c 6	34	64.2	608	7	US-11-024-959-315	Sequence 315, App
c 7	33	62.3	187	6	US-10-988-388-65	Sequence 65, App1
c 8	33	62.3	522	6	US-10-519-390-21	Sequence 21, App1
c 9	33	62.3	636	7	US-11-072-512-2449	Sequence 2449, Ap

Length: 13  
Matches: 6  
Conservative: 0  
Mismatch: 2  
Indels: 0

DB: 7 Gaps: 0 Pred. No.: 10.7 Length: 472  
 US-10-717-243-59 (1-28) x US-11-116-144-68 (1-13) Score: 35.00 Matches: 6  
 Qy 5 TGTAAACAGACTTCATTGGC 28 Percent Similarity: 100.0% Conservative: 1  
 / GENERAL INFORMATION: Best Local Similarity: 85.7% Mismatches: 0  
 / Publication No. US20050266423A1 Query Match: 66.0% Indels: 0  
 / DB: 129 LysIeLysercysPheThr 135 Gaps: 0

RESULT 2  
 US-11-098-68-11367  
 / Sequence 11367, Application US/110986866  
 / Publication No. US2006024656A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
 / TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
 / FILE REFERENCE: 095331-128001  
 / CURRENT APPLICATION NUMBER: US/11/098, 686  
 / CURRENT FILING DATE: 2005-04-04  
 / PRIOR APPLICATION NUMBER: PCT/US03/31318  
 / PRIOR FILING DATE: 2003-10-01  
 / PRIOR APPLICATION NUMBER: US 60/416,395  
 / PRIOR FILING DATE: 2002-10-04  
 / NUMBER OF SEQ ID NOS: 11433  
 / SOFTWARE: FastSEQ for Windows Version 4.0  
 / SEQ ID NO: 11367  
 / LENGTH: 445  
 / TYPE: PRT  
 / ORGANISM: Lawsonia intraceillularis  
 US-11-098-68-11367

Alignment Scores:  
 Pred. No.: 6.66 Length: 445  
 Score: 36.00 Matches: 6  
 Percent Similarity: 85.7% Conservative: 0  
 Best Local Similarity: 85.7% Mismatches: 1  
 Query Match: 67.9% Indels: 0  
 DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-098-686-11367 (1-445)  
 Qy 22 ATGAACTCTGTTTACATGT 2 Length: 445  
 / GENERAL INFORMATION: Score: 34.00 Matches: 5  
 / Publication No. US2005250180A1 Percent Similarity: 77.7% Conservative: 2  
 / APPLICANT: Jacobs, Kenneth Best Local Similarity: 55.6% Mismatches: 2  
 / APPLICANT: Spaulding, Vicki Current Application Number: US/10/689, 742 Indels: 0  
 / APPLICANT: Lavallie, Edward R Query Match: 64.2% Gaps: 0  
 / APPLICANT: Evans, Leisa A  
 / APPLICANT: Cheryl  
 / APPLICANT: Merberg, David  
 / APPLICANT: Treacy, Maurice  
 / APPLICANT: McCoy, John M  
 / APPLICANT: Racie, Leisa A  
 / APPLICANT: Evans, Cheryl  
 / APPLICANT: Merberg, David  
 / APPLICANT: Treacy, Maurice  
 / APPLICANT: Spaulding, Vicki  
 / TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 / FILE REFERENCE: 00766\_000091\_10 Length: 445  
 / CURRENT APPLICATION NUMBER: US/10/689, 742  
 / CURRENT FILING DATE: 2003-10-22  
 / PRIOR APPLICATION NUMBER: 09/746, 783  
 / PRIOR FILING DATE: 2000-12-21  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO: 68  
 / LENGTH: 472  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-689-142-68  
 Alignment Scores:

RESULT 3  
 US-10-689-742-68  
 / Sequence 68, Application US/10689742  
 / Publication No. US2005250180A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Jacobs, Kenneth Length: 326  
 / APPLICANT: Spaulding, Vicki Score: 34.00 Matches: 5  
 / APPLICANT: Lavallie, Edward R Percent Similarity: 77.7% Conservative: 2  
 / APPLICANT: Evans, Leisa A Best Local Similarity: 55.6% Mismatches: 2  
 / APPLICANT: Cheryl Current Application Number: US/10/689, 742 Indels: 0  
 / APPLICANT: Merberg, David Query Match: 64.2% Gaps: 0  
 / APPLICANT: Treacy, Maurice  
 / APPLICANT: McCoy, John M  
 / APPLICANT: Racie, Leisa A  
 / APPLICANT: Cheryl  
 / APPLICANT: Merberg, David  
 / APPLICANT: Treacy, Maurice  
 / APPLICANT: Spaulding, Vicki  
 / TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 / FILE REFERENCE: 00766\_000091\_10 Length: 326  
 / CURRENT APPLICATION NUMBER: US/10/689, 742  
 / CURRENT FILING DATE: 2003-10-22  
 / PRIOR APPLICATION NUMBER: 09/746, 783  
 / PRIOR FILING DATE: 2000-12-21  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO: 68  
 / LENGTH: 472  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-10-689-142-68  
 Alignment Scores:

RESULT 4  
 US-11-000-463-382  
 / Sequence 382, Application US/11000463  
 / Publication No. US20050266423A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Tang, Y. Tom  
 / APPLICANT: Liu, Chenghua  
 / APPLICANT: Abundi, Vinod  
 / APPLICANT: Chen, Rui-hong  
 / APPLICANT: Qian, Xiaohong B.  
 / APPLICANT: Wang, Zhiwei  
 / APPLICANT: Wehman, Tom  
 / APPLICANT: Zhang, Jie  
 / APPLICANT: Zhou, Ping  
 / APPLICANT: Cao, Yi-Cheng  
 / APPLICANT: Drmanac, Radmila T.  
 / TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 / FILE REFERENCE: 785C1P4CN  
 / CURRENT APPLICATION NUMBER: US/11/000,463  
 / CURRENT FILING DATE: 2004-11-29  
 / PRIOR APPLICATION NUMBER: 10/291,265  
 / PRIOR FILING DATE: 2002-11-08  
 / PRIOR APPLICATION NUMBER: PCT/US01/02623  
 / PRIOR FILING DATE: 2001-01-25  
 / PRIOR APPLICATION NUMBER: 09/922,279  
 / PRIOR FILING DATE: 2001-08-03  
 / PRIOR APPLICATION NUMBER: 09/491,404  
 / PRIOR FILING DATE: 2000-01-25  
 / PRIOR APPLICATION NUMBER: 09/617,746  
 / PRIOR FILING DATE: 2000-01-17  
 / PRIOR APPLICATION NUMBER: 09/631,451  
 / PRIOR FILING DATE: 2000-08-03  
 / PRIOR FILING DATE: 2000-09-15  
 / NUMBER OF SEQ ID NOS: 944  
 / SOFTWARE: FastSEQ for Windows Version 3.0  
 / SEQ ID NO: 382  
 / LENGTH: 326  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-11-000-463-382

RESULT 5  
 US-11-000-463-854  
 / Sequence 854, Application US/11000463  
 / Publication No. US20050266423A1

GENERAL INFORMATION

APPLICANT: Tang, Y. Tom  
Liu, Chenghua  
Asundi, Vinod

APPLICANT: Chen, Rui-hong  
Qian, Xiaohong B.

APPLICANT: Wang, Zhiwei  
Wehrman, Tom

APPLICANT: Zhang, Jie

APPLICANT: Zhou, Bing

APPLICANT: Cao, Yi-Cheng

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 78CIP4CN

CURRENT APPLICATION NUMBER: US/11/000,463

CURRENT FILING DATE: 2004-11-29

PRIOR APPLICATION NUMBER: 10/291,265

PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: PCT/US01/02623

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/922,279

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 09/617,746

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 09/633,870

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SEQ ID NO: 854

LENGTH: 326

TYPE: PRT

ORGANISM: Homo sapiens

US-11-000-43-854

Alignment Scores:

Pred. No.: 17.6 Length: 326

Score: 34.00 Matches: 5

Percent Similarity: 77.8% Conservative: 2

Best Local Similarity: 55.6% Mismatches: 2

Query Match: 64.2% Indels: 0

DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-024-959-315 (1-608)

Qy 28 GCCAAATGAGCTTGTTTACATC 2

Db 337 AlaLyGlyLyGlycBPhelysCys 345

RESULT 7

US-10-980-388-65

Sequence 65, Application US/10980388

Publication No. US20050255190A1

GENERAL INFORMATION:

APPLICANT: Vogeli, Gabriel  
APPLICANT: Paredi, Luis A.  
APPLICANT: Hiebsch, Ronald R.  
APPLICANT: Lind, Peter  
APPLICANT: Kaytes, Paul S.  
APPLICANT: Ruff, Valerie  
APPLICANT: Huff, Rita M.  
APPLICANT: Wood, Linda S.

TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App.

FILE REFERENCE: 00325-US1

CURRENT APPLICATION NUMBER: US/10/980,388

PRIOR APPLICATION NUMBER: US/09/791,932

PRIOR FILING DATE: 2004-11-02

PRIOR APPLICATION NUMBER: 60/184,305

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,304

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,303

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,397

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,247

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/188,880

PRIOR FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: 60/217,369

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/217,370

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/218,492

PRIOR FILING DATE: 2000-07-20

Remaining Prior Application data removed - See File Wrapper or PAM.

SOFTWARE: Patentin version 3.0

SEQ ID NO: 65

LENGTH: 187

TYPE: PRT

ORGANISM: Homo sapiens

US-10-980-388-65

Alignment Scores:

Pred. No.: 29 Length: 187

Score: 33.00 Matches: 5

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 62.3% Mismatches: 0

Query Match: 62.3% Indels: 0

DB: 6 Gaps: 0

RESULT 6

US-11-024-959-315

Sequence 315, Application US/11024959

Publication No. US20060010516A1

GENERAL INFORMATION:

APPLICANT: FORSTER, RICHARD L.

APPLICANT: CONNETT, MARIE B.

APPLICANT: EMERSON, SARAH JANE

APPLICANT: GRIGOR, MURRAY ROBERT

APPLICANT: HIGGINS, COLEEN M.

APPLICANT: HIGGINS, STEVEN TROY

APPLICANT: MAGUSIN, ANDREAS

APPLICANT: KODRZYCKI, BOB

TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS

FILE REFERENCE: 04463-0360

CURRENT APPLICATION NUMBER: US/11/024,959

PRIOR APPLICATION NUMBER: 60/533,036

PRIOR FILING DATE: 2003-12-30

NUMBER OF SEQ ID NOS: 782

SOFTWARE: Patentin version 3.3

US-10-717-243-59 (1-28) x US-10-980-388-65 (1-187)

Qy 16 TCTTGGTTACATGT 2  
Db 129 SerCysPheThrCys 133

RESULT 8

US-10-519-390-21  
Sequence 21, Application US/10519390  
Publication No. US20060008872A1

GENERAL INFORMATION:

APPLICANT: MEDEXGEN, Inc.

APPLICANT: LEE, Ha-k-sup

APPLICANT: YI, Ki-Wan

APPLICANT: KIM, Jae-Youn

APPLICANT: HEO, Youn-Hwa

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying proteins and the example mutagens

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/519,390

CURRENT FILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: KR10-2003-0051846

PRIOR FILING DATE: 2003-07-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Kopatentin 1.71

SEQ ID NO: 21

LENGTH: 522

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: M-CSF: 35th, 37th, 54th, 67th, 91st, 106th, 121st, 135th, 143rd, 145th, 146th, 148th, 150th, 152th, 154th, 156th, 158th, 160th, 162th, 164th, 166th, 168th, 170th, 172th, 174th, 176th, 178th, 180th, 182th, 184th, 186th, 188th, 190th, 192th, 194th, 196th, 198th, 200th, 202th, 204th, 206th, 208th, 210th, 212th, 214th, 216th, 218th, 220th, 222th, 224th, 226th, 228th, 230th, 232th, 234th, 236th, 238th, 240th, 242th, 244th, 246th, 248th, 250th, 252th, 254th, 256th, 258th, 260th, 262th, 264th, 266th, 268th, 270th, 272th, 274th, 276th, 278th, 280th, 282th, 284th, 286th, 288th, 290th, 292th, 294th, 296th, 298th, 300th, 302th, 304th, 306th, 308th, 310th, 312th, 314th, 316th, 318th, 320th, 322th, 324th, 326th, 328th, 330th, 332th, 334th, 336th, 338th, 340th, 342th, 344th, 346th, 348th, 350th, 352th, 354th, 356th, 358th, 360th, 362th, 364th, 366th, 368th, 370th, 372th, 374th, 376th, 378th, 380th, 382th, 384th, 386th, 388th, 390th, 392th, 394th, 396th, 398th, 400th, 402th, 404th, 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2980th, 2982th, 2984th, 2986th, 2988th, 2990th, 2992th, 2994th, 2996th, 2998th, 3000th, 3002th, 3004th, 3006th, 3008th, 3010th, 3012th, 3014th, 3016th, 3018th, 3020th, 3022th, 3024th, 3026th, 3028th, 3030th, 3032th, 3034th, 3036th, 3038th, 3040th, 3042th, 3044th, 3046th, 3048th, 3050th, 3052th, 3054th, 3056th, 3058th, 3060th, 3062th, 3064th, 3066th, 3068th, 3070th, 3072th, 3074th, 3076th, 3078th, 3080th, 3082th, 3084th, 3086th, 3088th, 3090th, 3092th, 3094th, 3096th, 3098th, 3100th, 3102th, 3104th, 3106th, 3108th, 3110th, 3112th, 3114th, 3116th, 3118th, 3120th, 3122th, 3124th, 3126th, 3128th, 3130th, 3132th, 3134th, 3136th, 3138th, 3140th, 3142th, 3144th, 3146th, 3148th, 3150th, 3152th, 3154th, 3156th, 3158th, 3160th, 3162th, 3164th, 3166th, 3168th, 3170th, 3172th, 3174th, 3176th, 3178th, 3180th, 3182th, 3184th, 3186th, 3188th, 3190th, 3192th, 3194th, 3196th, 3198th, 3200th, 3202th, 3204th, 3206th, 3208th, 3210th, 3212th, 3214th, 3216th, 3218th, 3220th, 3222th, 3224th, 3226th, 3228th, 3230th, 3232th, 3234th, 3236th, 3238th, 3240th, 3242th, 3244th, 3246th, 3248th, 3250th, 3252th, 3254th, 3256th, 3258th, 3260th, 3262th, 3264th, 3266th, 3268th, 3270th, 3272th, 3274th, 3276th, 3278th, 3280th, 3282th, 3284th, 3286th, 3288th, 3290th, 3292th, 3294th, 3296th, 3298th, 3300th, 3302th, 3304th, 3306th, 3308th, 3310th, 3312th, 3314th, 3316th, 3318th, 3320th, 3322th, 3324th, 3326th, 3328th, 3330th, 3332th, 3334th,

APPLICANT: Famodu, Omolayo O.  
 APPLICANT: Forge, Charlie  
 APPLICANT: Miao, Quo-Hua  
 TITLE OF INVENTION: cDNAs Encoding Polypeptides  
 FILE REFERENCE: BB-1365 US NA  
 CURRENT APPLICATION NUMBER: US/11/120,308  
 CURRENT FILING DATE: 2005-05-02  
 PRIOR APPLICATION NUMBER: US/10/078,770  
 PRIOR FILING DATE: 2002-02-19  
 PRIOR APPLICATION NUMBER: 09/614,188  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: 60/143,400  
 PRIOR FILING DATE: 1999-07-12  
 PRIOR APPLICATION NUMBER: 60/153,534  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: 60/161,223  
 PRIOR FILING DATE: 1999-10-22  
 PRIOR APPLICATION NUMBER: 60/159,878  
 PRIOR FILING DATE: 1999-10-15  
 PRIOR APPLICATION NUMBER: 60/157,401  
 PRIOR FILING DATE: 1999-10-01  
 PRIOR APPLICATION NUMBER: 60/143,419  
 PRIOR FILING DATE: 1999-07-12  
 PRIOR APPLICATION NUMBER: 60/143,409  
 PRIOR FILING DATE: 1999-07-12  
 NUMBER OF SEQ ID NOS: 196  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO: 76  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Zea mays  
 US-11-120-308-76

Alignment Scores:  
 Pred. No.: 49.9 Length: 36  
 Score: 32.00 Matches: 5  
 Percent Similarity: 75.0% Conservative: 1  
 Best Local Similarity: 62.5% Mismatches: 2  
 Query Match: 60.4% Indels: 0  
 DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-120-308-76 (1-36)

Qy 5 TGTAAAAACAGACTCATTTGGC 28  
 Db 7 CyBabntrArgIleLySpheGly 14

RESULT 12  
 US-10-995-561-605  
 Sequence 605, Application US/10995561  
 Publication No. US2005027205/A1

GENERAL INFORMATION  
 APPLICANT: CARGILL, Michele et al.  
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
 TITLE OF INVENTION: DETECTION AND USES THEREOF  
 FILE REFERENCE: CJO/01559  
 CURRENT APPLICATION NUMBER: US/10/995,561  
 CURRENT FILING DATE: 2004-11-24  
 NUMBER OF SEQ ID NOS: 85702  
 SOFTWARE: PastSeq for Windows Version 4.0  
 SEQ ID NO: 605  
 LENGTH: 127  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-995-561-605

Alignment Scores:  
 Pred. No.: 47.5 Length: 127  
 Score: 32.00 Matches: 4  
 Percent Similarity: 87.5% Conservative: 3  
 Best Local Similarity: 50.0% Mismatches: 1  
 Query Match: 60.4% Indels: 0

Job time : 12 secs

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; TYPE: PRT      ; ORGANISM: Homo sapiens
; US-11-132-285-61

Alignment Scores:
Pred. No.: 46.4 Length: 231
Score: 32.00 Matches: 5
Percent Similarity: 75.0% Conservative: 1
Best Local Similarity: 62.5% Mismatches: 2
Query Match: 60.4% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-132-285-61 (1-231)

Qy 25 AAAATGAGTCTGGTTACATGT 2
Db      ||| ::||||||| ||||| |
      57 LysCysGlnSerCysIleThrCys 64

RESULT 15
US-11-072-3294
; Sequence 3294, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKANATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUDRO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAROU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, TOSHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTONIKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3294
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3294

Alignment Scores:
Pred. No.: 46.4 Length: 238
Score: 32.00 Matches: 5
Percent Similarity: 83.3% Conservative: 0
Best Local Similarity: 83.3% Mismatches: 1
Query Match: 60.4% Indels: 0
DB: 7 Gaps: 0

US-10-717-243-59 (1-28) x US-11-072-512-3294 (1-238)

Qy 19 AAGTCPTGTTTACATGT 2
Db      ||| ::||||||| ||||| |
      128 LysSerCysPheCysCys 133

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 17, 2006, 09:46:44 ; Search time 4.8 Seconds  
(without alignments)  
112.253 Million cell updates/sec

Title: US-10-717-243-59  
Perfect score: 53  
Sequence: 1 CACATGTTAACAGACTCATTTGGC 28

Scoring table: BLOSUM62  
Xgapext 0.5  
Ygapext 0.5  
Fgapext 7.0  
Delop 7.0  
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing First 45 summaries

Command line parameters:

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-MODEL-frame+ n2p model1 -DEV=x1p
-Q=/abs/abs2_spoof -USF017243/runat_16022006_160652_2247/app query.fasta_1
-DB=PIR -QFT=fastran -SUFFIX=x1p -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40_cdi LIST=45
-DOCALIGN=1 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL
-OUTFILE=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=2000000000 -MAXLEN=2000000000 -HOST:abs02p
-USER=US1071743 @CGN 1-1-63 @runat_16022006_160652_2247 -NCPU=6 -ICPU=3
-NMAP -SCORES=0 -WAIT -DEBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -KGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : PIR\_B0:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	43	81.1	316	2	JT0753		rRNA N-glycosidase
c 2	40	75.5	133	2	S69759		hypothetical prote
c 3	37	69.8	391	2	T32156		hypothetical prote
c 4	37	69.8	1024	2	T41415		probable leucine D
c 5	37	69.8	1226	2	B844923		hypothetical prote
c 6	36	67.9	117	2	PH1542		IG H chain V
c 7	36	67.9	117	2	PH1152		hypothetical prote
c 8	36	67.9	381	2	T47144		hypothetical prote
c 9	35	66.0	107	2	T48759		hypothetical prote
c 10	35	66.0	108	2	H69334		hypothetical prote
c 11	35	66.0	245	2	C70090		hypothetical prote
c 12	35	66.0	379	2	A35878		class I major hist
c 13	35	66.0	406	2	B35878		class I major hist
c 14	35	66.0	516	2	A48678		activin receptor I

```
RESULT 1
JT0753
  rRNA N-glycosidase (EC 3.2.2.22) precursor - Gelonium multiflorum
  ;Alternative names: gelonin; type I ribosome-inactivating protein
  ;Species: Gelonium multiflorum
  ;Date: 30-Sep-1993 #sequence_change 20-Aug-1994 #text_change 09-Jul-2004
  ;Accession: JT0753; S16889
  ;R.Nolan, P.A.; Garrison, D.A.; Better, M.
  Gene 134, 223-227, 1993
  A;Title: Cloning and expression of a gene encoding gelonin, a ribosome-inactivating protein
  A;Reference number: JT0753; MUID: 94085781; PMID: 7916721
  A;Accession: JT0753
  A;Molecule type: mRNA
  A;Residues: 1-316 <NOL>
  A;Cross-references: UNIPROT:P31186; UNIPARC:UPI0000133948; GB:L12243; NID:9388633; PMID: 89326691; PMID:2733596
  B;Monocucchi, P.C.; Lazzarin, A.M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D.
  Int. J. Pept. Protein Res. 33, 263-267, 1989
  A;Title: N-terminal sequence of some ribosome-inactivating proteins.
  A;Reference number: S16489
  A;Accession: S16489
  A;Molecule type: protein
  A;Residues: 47-89, 'K', 91-92, 'D', <MON>
  A;Cross-references: UNIPARC:UPI0000177F26
  C;Function:
  C;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the
  C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
  C;Keywords: glycosidase; hydrolase
  F;1-46/Domain: signal sequence #status predicted <SIG>
  F;47-161/Domain: ribosomal RNA N-glycosidase #status predicted <SIG>
  F;53-294/Domain: rRNA N-glycosidase homology <RNG>
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## ALIGNMENTS

Score	Length	DB	ID	Description	Length:	Matches:
35	66.0	T27407			316	8
35	66.0	2278	1		316	8
35	65.1	T44425			316	8
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34	64.2	F86223			316	8
34	64.2	T17778			316	8
34	64.2	AD3163			316	8
34	64.2	LRG1			316	8
34	64.2	601884			316	8
34	64.2	GU2741			316	8
34	64.2	P69864			316	8
34	64.2	T50561			316	8
34	64.2	T26971			316	8
34	64.2	C56604			316	8
34	64.2	T26466			316	8
34	64.2	B15136			316	8
34	64.2	C87575			316	8
34	64.2	S69577			316	8
34	64.2	T05578			316	8
34	64.2	S73154			316	8
34	64.2	MN1HH3			316	8
34	64.2	T22430			316	8
34	64.2	D87282			316	8
34	64.2	T14900			316	8
34	64.2	T1490			316	8
34	64.2	G82524			316	8
34	64.2	S73154			316	8
34	64.2	62	1		316	8
34	64.2	77	1		316	8
34	64.2	1017	2		316	8
34	64.2	S67804			316	8
34	64.2	T11146			316	8
34	64.2	501	2		316	8
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34	64.2	S73154			316	8
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34	64.2	T14900			316	8
34	64.2	T1490			316	8
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34	64.2	1017	2		316	8
34	64.2	S67804			316	8
34	64.2	T11146			316	8
34	64.2	501	2		316	8
34	64.2	T26466			316	8
34	64.2	B15136			316	8
34	64.2	C87575			316	8
34	64.2	S69577			316	8
34	64.2	T05578			316	8
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34	64.2	T14900			316	8
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34	64.2	T22430			316	8
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34	64.2	MN1HH3			316	8
34	64.2	T22430			316	8
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34	64.2	T1490			316	8
34	64.2	G82524			316	8
34	64.2	S73154			316	8
34	64.2	MN1HH3		</td		

RESULT 4  
T41415  
probable leucine permease transcription regulator - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
Submitted to the EMBL Data Library, September 1998  
A;Reference number: Z221954  
A;Accession: T41415  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1024 <WOO>  
A;Cross-references: UNIPARC:UPI000006ADB9; PIDN:CAA21184.  
A;Experimental source: strain 9722h-; cosmid c576  
C;Genetics:  
A;Map position: 3  
A;Introns: 169/3; 251/1; 431/1

Alignment Scores:  
Pred. No.: 23.8  
Score: 37.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 69.8%  
DB: 2  
Length: 1024  
Matches: 6  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-717-243-59 (1-28) x T41415 (1-1024)  
Qy 10 AACAGACTTCATTGTTGG 27  
Db 781 AsnlysthrSerPheTrp 786

RESULT 5  
E84923  
hypothetical protein At2g48110 [imported] - Arabidopsis thaliana (mouse-ear cress)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; vanAken, S.E.; Tallon, L.;  
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: E84923  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1226 <STO>  
A;Cross-references: UNIPARC:Q9ZU78; UNIPARC:UPI00017A033; GB:AE002093; NID:96554175; PI  
C;Genetics:  
A;Map position: 2

Alignment Scores:  
Pred. No.: 23.6  
Score: 37.00  
Percent Similarity: 100.0%  
Best Local Similarity: 71.4%  
Query Match: 69.8%  
DB: 2  
Length: 1226  
Matches: 5  
Conservative: 2  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-717-243-59 (1-28) x E84923 (1-1226)  
Qy 22 ATGAGTCCTGTTACATGT 2  
Db 940 LeuArgSerCysPheThrCys 946

RESULT 6  
PH1442  
IG H chain V region (clone 7D8) - mouse (fragment)

Qy 2 ACATGAAAGAAAGACTTCATTGTC 28  
Db 19 SerCysArgThrHisPheHisPheGly 27

C;Species: *Mus musculus* (house mouse)  
 C;Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1542  
 R;Mukherjee, J.; Casadevall, A.; Scharff, M.D.  
 J.; Exp. Med. 177, 1105-1116, 1993  
 A;Title: Molecular characterization of the humoral responses to *Cryptococcus* neoformans  
 A;Reference number: PH1528; MUID:93210465; PMID:8459205  
 A;Accession: PH1542  
 A;Molecule type: mRNA  
 A;Residues: 1-117 <MDK>  
 A;Cross-references: UNIPARC:UPI00001768BC  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;14-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 43.7 Length: 117  
 Score: 36.00 Matches: 6  
 Percent Similarity: 87.5% Conservative: 1  
 Best Local Similarity: 75.0% Mismatches: 0  
 Query Match: 67.9% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x PH1542 (1-117)  
 T48759 hypothetical protein 13E11.70 [imported] - *Neurospora crassa*  
 C;Species: *Neurospora crassa*  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 19-May-2000  
 C;Accession: T48759  
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Branda, P.; Partmann, B.; Holland, R.; Nyakatura, A;Submitted to the Protein Sequence Database, April 2000  
 A;Reference number: Z24541  
 A;Accession: T48759  
 A;Molecule type: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-107 <SCH>  
 A;Cross-references: UNIPARC:UPI000017947A; EMBL:AU353820; GSPDB:GN00112; NCSP:13E11.70  
 A;Experimental source: cosmid contig 13E11; strain 74  
 C;Genetics:  
 A;Gene: NCSP:13E11.70  
 A;Map/Position: 2  
 C;Superfamily: *Neurospora crassa* hypothetical protein 13E11.70

Alignment Scores:  
 Pred. No.: 71.5 Length: 107  
 Score: 35.00 Matches: 6  
 Percent Similarity: 85.7% Conservative: 0  
 Best Local Similarity: 85.7% Mismatches: 1  
 Query Match: 66.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x T48759 (1-107)  
 H69834 hypothetical protein yhQ - *Bacillus subtilis*  
 C;Species: *Bacillus subtilis*  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: H69834  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Azevedo, V.; Berte, C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hullo, M.F.; Kurita, K.; Lapadic, A.; Lardinois, M.; Levine, A.; Liu, H.; Masuda, S.; Manue, Y.; Ogawa, K.; Ogiwara, A.; Ouduga, B.; Park, S.H.; Parco, V.; Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scantle, R.; Schreuter, R.; Scoffone, F.; Sekiguchi, J.; Seron, A;Submitted to the Protein Sequence Database, March 2000  
 A;Reference number: 224374  
 A;Accession: T47144  
 A;Status: preliminary

Alignment Scores:  
 Pred. No.: 43.7 Length: 117  
 Score: 36.00 Matches: 6  
 Percent Similarity: 87.5% Conservative: 1  
 Best Local Similarity: 75.0% Mismatches: 1  
 Query Match: 67.9% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x PH1552 (1-117)  
 T47144 hypothetical protein DKFZp761E1347.1 - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C;Accession: T47144  
 R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.  
 R;Submitted to the Protein Sequence Database, March 2000  
 A;Reference number: 224374  
 A;Accession: T47144  
 A;Status: preliminary

Alignment Scores:  
 Pred. No.: 43.7 Length: 117  
 Score: 36.00 Matches: 6  
 Percent Similarity: 87.5% Conservative: 1  
 Best Local Similarity: 75.0% Mismatches: 1  
 Query Match: 67.9% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x PH1552 (1-117)  
 T47144 hypothetical protein DKFZp761E1347.1 - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C;Accession: T47144  
 R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.  
 R;Submitted to the Protein Sequence Database, March 2000  
 A;Reference number: 224374  
 A;Accession: T47144  
 A;Status: preliminary



A;Accession: A48678  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-516 <CHI>  
 C;Cross-references: UNIPARC:UPI000007E5D2; GB:L22176; NID:9408504; PIDN:  
 C;Genetics:  
 A;Gene: FlyBase:put  
 A;Cross-references: FlyBase:FBgn003169  
 C;Keywords: ATP  
 P;200-494/domain: protein kinase homology <KIN>

Alignment Scores:  
 Pred. No.: 65.6 Length: 516  
 Score: 35.00 Matches: 6  
 Percent Similarity: 85.7% Conservative: 0  
 Best Local Similarity: 85.7% Mismatches: 1  
 Query Match: 66.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x A48678 (1-516)

Qy 25 AAAATGAGTCTTGTCTTACA 5  
 ||||| ||||| ||||| ||||| |||||  
 Db 83 LysMetLysGlyCysPheThr 89

RESULT 15  
 T27407 hypothetical protein Y75B8A.25 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Dec-2004  
 C;Accession: T27407  
 R;Barlow, K.  
 Submitted to the EMBL Data Library, November 1998

A;Reference number: Z20361  
 A;Accession: T27407

A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA

A;Residues: 1-570 <WIL>  
 A;Cross-references: UNIPROT:O9XW62; UNIPARC:UPI00000767FB; EMBL:AL033514; PIDN:CAA22109.  
 C;Genetics:  
 A;Gene: C8BP:Y75B8A.25  
 A;Experimental source: clone Y75B8A  
 A;Introns: 38/2; 128/2; 327/3; 389/3; 475/1; 518/3

Alignment Scores:  
 Pred. No.: 65.2 Length: 570  
 Score: 35.00 Matches: 6  
 Percent Similarity: 85.7% Conservative: 0  
 Best Local Similarity: 85.7% Mismatches: 1  
 Query Match: 66.0% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x T27407 (1-570)

Qy 2 ACATGAAAAACAAAGACTCAT 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 519 ThrCysIysProArgLeuHis 525

Search completed: February 17, 2006, 09:52:22  
 Job time : 26 SECs

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Db	206 LysMetLysAlaCysPheThrCys	213	Pred. No.:	2.1	Length:	382
<b>RESULT 2</b>						
Q68006	ARATH PRELIMINARY;	PRT;	Score:	45.00	Matches:	7
ID	Q68006;		Percent Similarity:	100.0%	Conservative:	1
AC			Best Local Similarity:	87.5%	Mismatches:	0
DT	25-OCT-2004 (TREMBLrel. 28, Created)		Query Match:	84.9%	Indels:	0
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		DB:	2	Gaps:	0
DE	Hypothetical protein At2g0640 (Fragment).					
GN	Name-At2g0640;					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OX	NON-TER 1					
NCBI_TaxID:3702;						
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RA	Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.					
RT	"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) submitted (SEP 2004) to the EMBL/GenBank/DBJ databases.					
RL	Submitted (SEP 2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AK176771; BAD43534.1; -; mRNA.					
PT	Hypothetical protein.					
SQ	SEQUENCE 365 AA; 41136 MW; F9C4B9A6A1C62DD9F CRC64;					
<b>Alignment Scores:</b>						
Pred. No.:	2.09	Length:	365	Pred. No.:	2.1	Length:
Score:	45.00	Matches:	7	Score:	45.00	Length:
Percent Similarity:	100.0%	Conservative:	1	Percent Similarity:	100.0%	383
Best Local Similarity:	87.5%	Mismatches:	0	Best Local Similarity:	87.5%	
Query Match:	84.9%	Indels:	0	Query Match:	84.9%	
DB:	2	Gaps:	0	DB:	2	Gaps:
US-10-717-243-59 (1-28) x Q68006_ARATH (1-355)						
Qy	25 AAAATGAGCTCTGTTACATGT 2					
Db	219 LysMetLysAlaCysPheThrCys 226					
<b>RESULT 3</b>						
Q67X57	ARATH PRELIMINARY;	PRT;	Score:	382 AA.		
ID	Q67X57;					
AC						
DT	25-OCT-2004 (TREMBLrel. 28, Created)					
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)					
DE	Hypothetical protein At2g0640 (Fragment).					
GN	Name-At2g0640;					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OX	NON-TER 1					
NCBI_TaxID:3702;						
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RA	Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.					
RT	"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) submitted (SEP 2004) to the EMBL/GenBank/DBJ databases.					
RL	Submitted (SEP 2004) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AK17641; BAD4504.1; -; mRNA.					
PT	Hypothetical protein.					
SQ	SEQUENCE 382 AA; 43170 MW; 9FC42DD001F22226FE CRC64;					
<b>Alignment Scores:</b>						
Pred. No.:	2.1	Length:	382	Pred. No.:	2.1	Length:
Score:	45.00	Matches:	7	Score:	45.00	Length:
Percent Similarity:	100.0%	Conservative:	1	Percent Similarity:	100.0%	383 AA.
Best Local Similarity:	87.5%	Mismatches:	0	Best Local Similarity:	87.5%	
Query Match:	84.9%	Indels:	0	Query Match:	84.9%	
DB:	2	Gaps:	0	DB:	2	Gaps:
US-10-717-243-59 (1-28) x Q58FY4_ARATH (1-383)						
Qy	25 AAAATGAGCTCTGTTACATGT 2					
Db	237 LysMetLysAlaCysPheThrCys 244					
<b>RESULT 4</b>						
Q58FY4	ARATH PRELIMINARY;	PRT;	Score:	383 AA.		
ID	Q58FY4;					
AC						
DT	10-MAY-2005 (TREMBLrel. 30, Created)					
DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)					
DE	Hypothetical protein.					
GN	ORFnames-At2g0640;					
OS	Arabidopsis thaliana (Mouse-ear cress).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OX	NON-TER 1					
NCBI_TaxID:3702;						
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RA	Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.					
RT	"Cloning and sequencing of cDNAs for hypothetical genes from chromosome 2 of Arabidopsis."					
RL	Plant Physiol. 130:2118-2128 (2002).					
RN	[2]					
RP	NUCLEOTIDE SEQUENCE.					

RA Xiao Y., Smith S.R., Ishmael N., Kumar N., Redman J., Riedmiller S., Utterback T., Whitehead C.A., Fraser C.M., Town C.D.; Submitted (Oct 2002) to the EMBL/GenBank/DBJ databases.

RL DR EMBL; AA168999; AA011670.1; -; mRNA.

KW Hypothetical Protein.

SQ SEQUENCE 383 AA; 43206 MW; 9993C935E4BF1C99 CRC64;

Alignment Scores:

Pred. No.:	2.1	Length:	383
Score:	45.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	87.5%	Mismatches:	0
Query Match:	84.9%	Indels:	0
DB:	2	Gaps:	0

US-10-717-243-59 (1-28) x Q8GUT1\_ARATH (1-383)

Qy 25 AAATGAGTCAGTACATG 2

Db 237 LysMetLysAlaCysPheThrCys 244

RESULT 6

RP_GELMU	RP_GELMU	STANDARD	PRT	316 AA.
ID	ID			
AC	P33186			
DT	01-OCT-1993	(Rel. 27, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DT	10-MAY-2005	(Rel. 47, Last annotation update)		
DE	Ribosome-inactivating protein gelonin precursor	(EC 3.2.2.22)	(rRNA N-glycosidase).	
GN	Name=GLN;			
OS	Gelonium multiflorum (Euphorbiaceae himalaya).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;			
OC	Geloniaceae; Gelonium.			
OX	NCBI_TaxID=3979;			
RP	NUCLEOTIDE SEQUENCE			
RX	Medline:94085781; PubMed:7916721; DOI=10.1016/0378-1119(93)90097-M;			
RA	Nolan B.A., Garrick D.A., Better M.,			
RT	"Cloning and expression of a gene encoding gelonin, a ribosome-			
RT	inactivating protein from Gelonium multiflorum.";			
RL	Gene 134:223-227(1993).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 47-93.			
RX	Medline:89326691; PubMed:2753596;			
RA	Montecuccchi P.-C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.;			
RT	"N-terminal sequence of bone ribosome-inactivating proteines".			
RL	Int. J. Pept. Protein Res. 33:263-267(1999).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).			
RX	Medline:95333189; PubMed:7608981;			
RA	Kannan K.K., Nair B., Satyanurthy P., Misquith S., Surolia A., RT	"X-ray structure of gelonin at 1.8-A resolution."		
RL	J. Mol. Biol. 250:368-380 (1995).			
CC	-; CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific adenosine on the 28S rRNA.			
CC	-; SUBUNIT: Homodimer.			
CC	-; SIMILARITY: Belongs to the ribosome-inactivating protein family.			
CC	Type 1 RIP subfamily.			
CC	CC	CC	CC	CC
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	DR EMBL; I12243; AA16312.1; -; mRNA.			
DR	PIR; JF0753;			

DR	PROSITE; PS50162; RECA_2; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 465 AA; 51817 MW; 1472774706CD287B CRC64;			
Alignment Scores:				
Pred. No.:	5.86	Length: 465		
Score:	43.00	Matches: 7		
Percent Similarity:	88.9%	Conservative: 1		
Best Local Similarity:	77.8%	Mismatches: 1		
Query Match:	81.1%	Indels: 0		
DB:	2	Gaps: 0		
US-10-717-243-59 (1-28) x Q89017_CLOTE (1-465)				
Qy	28 GCAATGAGTCCTGTTACATGT 2			
	:     :     :     :			
Db	13 AlaLysIleLysSerCysPheValCys 21			
RESULT 8				
Q5JS06_HUMAN PRELIMINARY;	PRT; 109 AA.			
Q5JS06_HUMAN PRELIMINARY;	PRT; 109 AA.			
AC	Q5JS06; HUMAN PRELIMINARY;			
DT	10-MAY-2005 (TREMBLrel. 30, Created)			
DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)			
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)			
DE	Zinc Finger, DHHC domain containing 14 (Fragment).			
ORFName=R3-49LC-1;	Length: 109 AA.			
OS	Homo sapiens (Human) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
NCBI_TaxID=9606;				
RN	NUCLEOTIDE SEQUENCE.			
RA	Johnson C;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Almeida J;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL40328; CAI39700_1; -; Genomic DNA.			
DR	EMBL; AL133510; CAI12854_1; -; Genomic DNA.			
DR	EMBL; AL133510; CAI139700_1; ; JOINED; Genomic DNA.			
DR	EMBL; AL40328; CAI12854_1; ; JOINED; Genomic DNA.			
GO	GO:0046872; Fatty acid binding; IBA.			
DR	InterPro; IPR01594; Znf DHHC.			
PFam	PF01529; zf-DHHC; 1.			
ProDom	PS003041; Znf DHHC; 1.			
PROSITE	PS50216; Zf-DHHC; 1.			
DR	NON_TER 1_1			
FT	NON_TER 1_1			
FT	SEQUENCE 109 AA; 12147 MW; 415F90439F4866DF CRC64;			
Qy	25 AAAATGAGTCCTGTTACATGT 2			
	:     :     :     :			
Db	20 LysLeuLysSerCysPheThrCys 27			
RESULT 9				
Q5Y5T2_MOUSE PRELIMINARY;	PRT; 253 AA.			
ID	Q5Y5T2_MOUSE PRELIMINARY;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DT	DHHC-containing protein 18.			
DB	DBP; DHHC18; Name=Dhmc18;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10990;				
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
STRAIN=C57BL/6J; TISSUE=Brain;				
RC	Fukata M.; Fukata Y.; Breit D.S.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
RT	"DHHC-containing protein."			
RL	DR			
DR	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
MGII; MGII:35227792; Zdhhc18.				
GO; GO:0046872; F-metal ion binding; IBA.				
DR	InterPro; IPR003006; 19 MHC.			
DR	InterPro; IPR001594; Znf DHHC.			
PFam; PF01529; zf-DHHC; 1.				
DR	ProDom; PD00341; Znf DHHC; 1.			
DR	DR			
DR	PROSITE; PS00390; IG_MHC; UNKNOWN_1.			
DR	PROSITE; PS50216; Zf-DHHC; 1.			
SEQUENCE 253 AA; 27743 MW; 7FA252BA74A17E8 CRC64;				
Alignment Scores:				
Pred. No.:	41.7	Length: 253		
Score:	39.00	Matches: 6		
Percent Similarity:	87.5%	Conservative: 1		
Best Local Similarity:	75.0%	Mismatches: 1		
Query Match:	73.6%	Indels: 0		
DB:	2	Gaps: 0		
US-10-717-243-59 (1-28) x Q5Y5T2_MOUSE (1-253)				
Qy	25 AAAATGAGTCCTGTTACATGT 2			
	:     :     :     :			
Db	55 LysLeuLysSerCysPheThrCys 62			
RESULT 10				
Q9SS44_GELMU PRELIMINARY;	PRT; 258 AA.			
ID	Q9SS44_GELMU PRELIMINARY;			
AC	Q9SS44;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	rRNA -glycosidase (EC 3.2.2.22) (rRNA N-glycosidase).			
OS	Gelonium multiflorum (Euphorbiaceae himalaya).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embophytida; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Gelinaceae; Gelinium.			
OC	NCBI_TaxID=3979;			
RN	[1]			
RP	PROTEIN SEQUENCE.			
MEDLINE=16006751; PubMed=7553224;				
RX	Rosenblum M.G.; Rohr W.A.; Beattie K.L.; Beattie W.G.; Marks W.;			
RA	Toman P.D.; Cheung L.;			
RA	"Amino acid sequence analysis, gene construction, cloning, and expression of Gelonin, a toxin derived from Gelonium multiflorum." J. Interteron Cytokine Res. 15:54-55 (1995).			
RL	DR			
DR	HSSP; P0989; 1MRJ.			
DR	GO; GO:0016787; F-hydrolase activity; IBA.			
DR	DR			
DR	GO; GO:0030598; rRNA N-glycosidase activity; IBA.			
DR	GO; GO:0006952; P-defense response; IBA.			
DR	GO; GO:0017148; P-negative regulation of protein biosynthesis; IBA.			
DR	GO; GO:0094052; P-pathogenesis; IBA.			
DR	InterPro; IPR01574; RIP.			
PFam; PF0161; RIP.				
DR	PRINTS; PR00346; SHIGARICIN.			
DR	HYDROLASE; PS00075; SHIGA RICIN.			
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.			
SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;				
SQ				

Alignment Scores:						
Pred. No. :	41.7	Length:	258			
Score:	39.00	Matches:	7			
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Missmatches:	0			
Query Match:	73.6%	Indels:	0			
DB:	2	Gaps:	0			
US-10-717-243-59 (1-28) x Q9S9B4_GELMU (1-258)						
Qy	8 AAAACAGACTTCAATTCTGGC 28					
Db	111 LysThrArgLeuHisPheGly 117					
RESULT 11						
Q5JYH0 HUMAN PRELIMINARY;		PRT;	303 AA.			
ID Q5JYH0; HUMAN PRELIMINARY;						
AC AC						
DT DT	10-MAY-2005 (TREMBLrel. 30, Created)					
DR DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)					
DR DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)					
DE Zinc finger, DHHC domain containing 18.						
NAME ZDHHC18; ORFNames=RPI-500C43-3-001;						
OS Homo sapiens (Human);						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;						
OC Homo.						
OX NCBI_TaxID=9606;						
RN [1]						
RP NUCLEOTIDE SEQUENCE.						
RA Whitehead S.;						
DR Submitted (May-2005) to the EMBL/GenBank/DBJ databases.						
DR EMBL; AL034380; CAI21624.1; -; Genomic DNA.						
DR GO:0046872; F:metal ion binding; IEA.						
DR InterPro; IPR003006; Ig_MHC.						
DR InterPro; IPR001594; Znf_DHHC.						
DR Pfam; PF01529; zf-DHHC; 1.						
DR ProDom; PDO03041; Znf_DHHC; 1.						
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.						
DR PROSITE; PS50216; zf_DHHC; 1.						
DR PROSITE; PS50216; zf_DHHC; 1.						
SEQ ID 33367 MW; C13A27BF2CC6C22ES CRC64;						
Alignment Scores:						
Pred. No. :	42.3	Length:	303			
Score:	39.00	Matches:	6			
Percent Similarity:	87.5%	Conservative:	1			
Best Local Similarity:	75.0%	Missmatches:	1			
Query Match:	73.6%	Indels:	0			
DB:	2	Gaps:	0			
US-10-717-243-59 (1-28) x Q5JYH0_HUMAN (1-303)						
Qy	25 ANATGAGTCTGTTACATGT 2					
Db	105 LysLeuIysTyrCysPheThrCys 112					
RESULT 12						
Q7PQ26 ANOGA PRELIMINARY;		PRT;	305 AA.			
ID Q7PQ26; ANOGA PRELIMINARY;						
AC AC						
DT DT	01-MAR-2004 (TREMBLrel. 26, Created)					
DT DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)					
DT DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
DB ENSANGP000000009567 (Fragment).						
DR ORFNames=ENSG000000007478;						
OS Anopheles gambiae str. PEST.						
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;						
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;						
OC Anophelinidae; Anophelinae.						
OX NCBI_TaxID=180454;						
RP NUCLEOTIDE SEQUENCE.						

CC Preliminary data.  
 DR EMBL; CAAE01014594; CAG00265.1; -; Genomic\_DNA.  
 PT NON-TER 329 329  
 SQ SEQUENCE 329 AA; 36192 MW; B045DCCE5541E538 CRC64;

Alignment Scores:  
 Pred. No.: 42.7 Length: 329  
 Score: 39.00 Matches: 6  
 Percent Similarity: 87.5% Mismatches: 1  
 Best Local Similarity: 75.0% Indels: 0  
 Query Match: 73.6% Gaps: 0  
 DB: 2

US-10-717-243-59 (1-28) x Q4SGGG7\_TETNG (1-329)

Qy 25 AAAATGAGCTCTGTTACATGT 2  
 DR [1::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE NEW1 domain containing protein.  
 GN Name=Zdhhc14;  
 OS Mus musculus (Mouse).  
 OC Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Mus.  
 NCBI\_TaxID=10909; OX

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALB/C; TISSUE=Adipose;  
 RA Guo J.H.; Chen L.; Yu L.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ/GenBank/DBJ databases.  
 DR Ensembl; ENSMUSG0000034265; Mus musculus.  
 DR MGI; MGI:2653229; Zdhhc14.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR InterPro; IPR001594; Znf\_DHHC.  
 DR Pfam; PF01529; Zf\_DHHC; T.  
 DR ProDom; PD00341; Znf\_DHHC; 1.  
 DR PROSITE; PS5016; ZF\_DHHC; 1.  
 DR SEQUENCE 384 AA; 41836 MW; 5E1BB23A22B22A9B CRC64;

Alignment Scores:  
 Pred. No.: 43.3 Length: 384  
 Score: 39.00 Matches: 6  
 Percent Similarity: 87.5% Conservative: 1  
 Best Local Similarity: 75.0% Mismatches: 1  
 Query Match: 73.6% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q8CFNO\_MOUSE (1-384)

Qy 25 AAAATGAGCTCTGTTACATGT 2  
 Db 58 LysLeuLysTyrCysPheThrCys 65

Search completed: February 17, 2006, 09:51:29  
 Job time : 150.5 secs

RP NUCLEOTIDE SEQUENCE.  
 RA Johnson C.; submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RL [2]

RP NUCLEOTIDE SEQUENCE.  
 RA Almeida J.; submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL450328; CAI19701.1; -; Genomic\_DNA.  
 DR EMBL; AL133510; CAI142855.1; -; Genomic\_DNA.  
 DR EMBL; AL450328; CAI19701.1; JOINED; Genomic\_DNA.  
 DR GO; GO:0046872; F: metal ion binding; IEA.  
 DR InterPro; IPR001594; Znf\_DHHC.  
 DR Pfam; PF01529; Zf\_DHHC; 1.  
 DR ProDom; PD003041; Znf\_DHHC; 1.  
 DR PROSITE; PS50216; ZF\_DHHC; 1.  
 FT NON-TER 1  
 SQ SEQUENCE 371 AA; 40291 MW; A45CE211B9FE4F4B CRC64;

Alignment Scores:  
 Pred. No.: 43.1 Length: 371  
 Score: 39.00 Matches: 6  
 Percent Similarity: 87.5% Conservative: 1  
 Best Local Similarity: 75.0% Mismatches: 1  
 Query Match: 73.6% Indels: 0  
 DB: 2 Gaps: 0

US-10-717-243-59 (1-28) x Q5US05\_HUMAN (1-371)

Qy 25 AAAATGAGCTCTGTTACATGT 2  
 Db 46 LysLeuLysTyrCysPheThrCys 53

RESIDUE 15  
 Q8CFNO\_MOUSE  
 ID Q8CFNO\_MOUSE PRELIMINARY;  
 AC Q8CFNO;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)